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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 FLKNGATQGWDAPQEVPYAYQGNVWVGYDNIKSFDIKAQWLKHNKFGGAMVWAIDLDDFT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
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                            288 FLKNGATQGWDAPQEVPYAYQGNVWVGYDNIKSFDIKAQWLKHNKFGGAMVWAIDLDDFT 347
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325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Macrozyme
APPLICANT: Macrozyme
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Kolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
TITLE OF INVENTION: WHICH mucus is involved or infection diseases
CURRENT APPLICATION NUMBER: US/10/004,219B
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
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                                                                                                                            ---STLKKALGLOSASCTAPAQPIEPITAAPSGS 390
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                                                                                                  385 G-HCGP-KNPLLNKVHNMINGDEKNSPECILGPSTTTPTTTTPTTTPTTPTTPS 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.8%; Score 708.5; DB 14; Length 476; Best Local Similarity 35.9%; Pred. No. 8.6e-44; Matches 149; Conservative 75; Mismatches 154; Indels 37;
                                                                                                                                                                                                                                                                    Sequence 1, Application US/10004219B
Publication No. US20030087414A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                348 GTFCNOGKFPLI----
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Search completed: March 22, 2004, 07:45:51 Job time : 115.53 secs

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March 22, 2004, 06:42:54 ; Search time 44.7332 Seconds (without alignments) 640.518 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                      389414 seqs, 51625971 residues
                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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3107
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Issued_Patents_AA:*

(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 15, Appl Sequence 21, Appl Sequence 35, Appl Sequence 36, Appl Sequence 2, Appl Sequence 2, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 4, Appli Sequence 2, M. Sequence 4, M. Sequence 2, M. Sequence 2, M. Sequence 6, M. Sequence 6, M. Sequence 4, M. Sequence 4, M. Sequence 14, M. Sequence 115, Sequence 115, Sequence 115, M. Sequence 115 Description US-09-292-225-18 US-09-292-225-18 US-09-292-225-31 US-09-292-225-31 US-09-292-225-31 US-09-292-225-41 US-09-292-225-41 US-09-29-225-41 US-09-65-814-12 US-09-65-814-14 US-09-545-814-35 US-09-545-814-35 US-09-545-814-35 US-09-151-011-4 US-09-151-011-4 US-09-151-011-6 US-09-151-011-6 US-09-151-011-6 US-09-151-011-6 US-09-151-011-6 US-09-151-011-6 US-09-267-574-2 US-09-39-198A-4 US-09-39-198A-4 US-09-39-198A-4 US-09-267-574-4 US-09-267-574-4 US-09-267-574-4 US-09-267-574-4 SUMMARIES Query Match Length 3107 3107 3107 22542 2254 22542 22542 22542 22542 22542 22542 22542 22542 22542 22542 2254 Result

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Gaps

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Length 0; Indels

Query Match 100.0%; Score 3107; DB 4; Best Local Similarity 100.0%; Pred. No. 6.5e-241; Matches 555; Conservative 0; Mismatches 0;

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1 MKTIYAILSIMACIGLANASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK

MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK

CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY

CTHIANGFAKI DEYKYTI QVFDPYQDDNHNSWEKRGYER FNNLRLKNPELTTMI SLGGWY

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EGSEKYSDWAANPTYRQQFIQSVLDFLQEYKPDGLDLDWEYPGSRLGNPKIDKQNYLALV

EGSEKYSDWAANPTYRQOPIOSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV

120 120 180 241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA

RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNA

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721.5	721.5	672.5	650	630	630	630	420	419.5	417	412	412	411	411	403.5	403.5	403.5
7 7 8 8 7 8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

RESULT 1		
US-09-292-225-15		
; Sequence 15, Application US/0929225		
; Patent No. 6455686		
; GENERAL INFORMATION:		
; APPLICANT: McCall, Catherine A.		
; APPLICANT: Hunter, Shirley Wu		
; APPLICANT: Weber, Eric R.		
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTE:	ID MOLECULES,	PROTE
; TITLE OF INVENTION: AND USES THEREOF		
; FILE REFERENCE: AL-2-C3		
; CURRENT APPLICATION NUMBER: US/09/292,225		
CURRENT FILING DATE: 1999-04-15		
; EARLIER APPLICATION NUMBER: 60/098,909		
; EARLIER FILING DATE: 1998-09-02		
; EARLIER APPLICATION NUMBER: 60/085,295		
; EARLIER FILING DATE: 1998-05-13		
; EARLIER APPLICATION NUMBER: 60/098,565		
; BARLIER FILING DATE: 1998-04-17		
; EARLIER APPLICATION NUMBER: 09/062,013		
; EARLIER FILING DATE: 1998-04-17		
; NUMBER OF SEQ ID NOS: 49		
; SOFTWARE: Patentin Ver. 2.0		
; SEO ID NO 15		
; LENGTH: 555		
; TYPE: PRT		
; ORGANISM: Dermatophagoides farinae		
US-09-292-225-15		

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PGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENPYGHNAPLYKRPDETDELHTYFNVN 240
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                                                241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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                                                                                                                                               301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
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                                                                                                            KGMSPPGFISGEEGVLSYIELCOLFOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
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GRENEAL INFORMATION:
APPLICANT: MCCall, Catherine A.
APPLICANT: MCCall, Catherine A.
APPLICANT: WCALL, Shirley Wu
I APPLICANT: WCALL
I STRIEMER.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROT
TITLE OF INVENTION: AND USES THEREOF
FILE REFRENCE: AL.2-C3
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATCHING DATE: 1998-04-17
I ERRITH FILING DATE: 1998-04-17
SEQ ID NO 21
LENGTH: 336
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Sequence 21, Application US/09292225
Patent No. 6455686
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Dermatophagoides farinae US-09-292-225-21
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Patent No. 645566

RENERAL INPORMATION:
APPLICANT: Muccall, Catherine A.
APPLICANT: Muccall, Catherine A.
APPLICANT: Muccall, Catherine A.
APPLICANT: Weber, Eric R.
TILLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOW USER THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,505
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
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                                                                                 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                                                                                                                                  301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
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; Pred. No. 6.5e-241;
0; Mismatches 0;

; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18

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Best Local Similarity 100.0
Matches 555, Conservative
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TITLE OF INVENTION: MOYEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE PREPARENCE: AL-2-C3
CURRENT APPLICATION NUMBER: 60/096,295
EARLIER APPLICATION NUMBER: 60/096,295
EARLIER APPLICATION NUMBER: 60/096,295
EARLIER PILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/096,565
EARLIER FILING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
SOFTWARE: PALENTING DATE: 1998-04-17
SOFTWARE: PALENTING DATE: 1998-04-17
SOFTWARE: PALENTING DATE: 209
SOFTWARE: PALENTING DATE: 209
EARLIER FILING DATE: 1998-04-17
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                                                                                      301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300
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81.8%; Score 2542; DB 4; Length 50
Best Local Similarity 81.7%; Pred. No. 1.1e-195;
Matches 456; Conservative 24; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38
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Sequence 35, Application US/0929225

Sequence 35, Application US/0929225

Patent No. 6455666

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: HURCE, Shirley Wu
APPLICANT: HURCE, Shirley Wu
APPLICANT: HURCE, Shirley Wu
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
FILE REFERENCE: AL-2-C3
CURRENT FILING ADTE: 1999-04-15
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
EARLIER FILING DATE: 1998-05-03
EARLIER FILING DATE: 1998-05-13
EARLIER REPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER PELLING DATE: 1998-04-17
EARLIER PELLING DATE: 1998-04-17
SARLIER PELLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOUTHARE PELENTING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 35
LENGTH: 509
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                                                                    241 YIWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300
                                                                                                                                            BLCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
                                                                                                                                                                                                 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360
                                                                                                                                                                                                                                                          NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGBSTTTPTTTTTTTTTTTTTTTT 439
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Best Local Similarity 81.7%; Pred. No. 1.1e-195;
Matches 456; Conservative 24; Mismatches 26; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35
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363 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTTFFSTTTPT----- 415
                                                                             CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
                                                                                                                   303 COLFOKBEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362
                                                                                                                                                           DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTPTTPF 441
                                                                                                                                                                                                                                                                         ------PTTTDSTSETPKYTTYID 433
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                                                                                                                                                                                                                                                                                                                 502 GHLIKCYKEGDIPHPINIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
                                                                                                                                                                                                                                                                                                                                       442 TITPSPITTPSPITPTITPSPITPTTPTPTPAPITSTPSPITTEHTSETPKYITYVD
                             243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPFGFITGEEGVLSYIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/524,051
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 25,262
REFERENCE/DOCKET NUMBER: 22875-A
TELEPHONE: (816)474-9050
TELEPHONE: (816)474-9057
TELEFRENCE: 434-363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%; Score 838.5; DB 2; 35.4%; Pred. No. 4.8e-59; tive 79; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 434-363
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acids
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    MOLECULE TYPE: protein
US-08-524-051-2
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Best Local Simi
Matches 208;
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Patent No. 645566

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: Meber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, CURRENT PLING DATE: 1999-04-15
CURRENT PLING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098, 99
EARLIER PILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098, 565
EARLIER PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
LENGTH 490
                                                                                   301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                                                                                                                                                               361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420
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PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300
                                                                                                                                       KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
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                                                                                                                                                                                                                                                                                             481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                                                                                                                                                                                                                                                                                                                     435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORGANISM: Dermatophagoides farinae US-09-292-225-41
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Best Local Similarity 82.5%
Matches 443; Conservative
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US-09-292-225-41
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                    KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
                                                                             KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
                                                                                                                                       |||||| : : |||| : 231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFT 289
                                                                                                                                                                                                                                         291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                                                                                                                                                                                                                                                                      290 NKEAGGGDPAPYTNATGF-----WAYXEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342
                                                                                                                                                                                                                                                                                                     WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
                                                                                                                                                                                                                                                                                                                      343 WVGYEDPRSVEIKANMIKQKGYLGAMIWALDMDDFQGLCGEKNPLIKILHKHMS----- 396
                                                                                                                                                                                                                                                                                                                                                                  FECILGPSTTTPTPTTPTTPTTPT -----TTPTTPS-----PTTPTTPSPTTPTPSPTTPSP 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYSDMAANPTYRQOPIOSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVF-PTENE-------VDGSEI 497
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                                                                                                                                                                                 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 -CNSDQDYIPDKXHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eryant, Peter J.
APPLICANT: Kawamura, Kazuo
TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 07306/015001
CURRENT APPLICATION NUMBER: US/09/052,778A
CURRENT APPLICATION NUMBER: 1998-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score 838.5; DB 3;
35.4%; Pred. No. 4.8e-59;
live 79; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09052778A; Patent No. 6060590; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.4
Matches 208; Conservative
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ORGANISM: Manduca sexta
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US-09-052-778-16
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                                   231 LYKRPHD-OWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPPYGRSFTLSAGNNNYGLGTFI 289
                                                                                                                                                                                                                             291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                                                                                                                                                                                                                                                                                  290 NKEAGGGDPAPYTNATGF-----WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342
                                                                                                                                                                                                                                                                                                                                             WYGYDDLASISCKLAFLKELGVSGVMYWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 FECILGPSTTTPTPTTTTPTTPT-----TTPTTPS-----PTTPTTTPSPTTPTFSP 456
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Patent No. 6416977
GENERAL INFORMATION:
TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF
PILE REPERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT APPLICATION NUMBER: 06/128,833
PRIOR PILING DATE: 1999-04-09
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Best Local Similarity 34.6%; Pred. No. 3.6e-57;
Matches 198; Conservative 94; Mismatches 205; Indels
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; ORGANISM: Ctenocephalides felis
US-09-545-814-2
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SEQ ID NO 2
LENGTH: 583
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US-09-545-814-2
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us-09-662-293-15.rai

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Sequence 32, Application US/09545814 Patent No. 6416977 GENERAL INFORMATION: APPLICANT: Becher, Anna M.
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Best Local Similarity 34.64
Matches 198; Conservative
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US-09-545-814-32
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YRRPHD-QYAYEKLNVNDGLQLWVDMGCPANKLVVGVPFYGRSFTLSNSNKDYRLGTYIN 295
                                                    296 KEAGGGEPGPYTNATGFISYYEICLEVDDPSKGWTKKWDEHGKVPYAYKGNQWVGYEDPK 355
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Becher, Anna M.
TITLE OF INVENTION: PLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                              PAKGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLA
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Patent No. 6416977
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------TTTEHHHHHHEEEKPSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 511
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                                                                                                                                      412 SRITPRPEWAKPPSTPSQEP-DDTPYIPTHAPKPSRKPTRKPKPT-TTTVAATTPVAT 468
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CURRENT APPLICATION NUMBER: US/09/545,814

CURRENT FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 60/128,833

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 2.1
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34.6%; Pred. No. 7e-57;
cive 93; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                      ::|| ::DCNKYYRC-----VHGBAVLFTCREGTVY 535
                                                                                                                                                                                                                                                                                                       518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Tagged Ctenocephalides felis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 HVPELCELLDAIHVMSYDLRGNWAGFADTHSPLYRRPHD-QYAYEKLNVNDGLQLWVDMG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 CPANKLVVGVPFYGRSFTLSNSNKDYRLGTYINKEAGGGEPGPYTNATGFISYYEICLEV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | : | : | : | : | 359 QGVCSDDKHTAVIMHDYM----KONIVPEFDSSRITPRPEWAKPPSTPSQEP-DDTPYI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPTPAPTTSTPSPTTTE----HTSETP-----KYTTYVDGHLIKCYKEGDIPHPT 517
                       --TITEHHHHHEEKPSEODNOVGSODITAID---VDCSOEDYLPH-E 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKF 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYIELCQLF 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
                                                                                                                                                                                                                        APPLICANT: Becher, Anna M.

TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: FC-5-C1 CURRENT APPLICATION NUMBER: US/09/545,814

CURRENT APPLICATION NUMBER: 60/128,833

PRIOR PELING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLDLDWEYPGSR-LGNPKIDKONYLALVRELKDAFEPHG--YLLTAAVSPGKDKIDRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 811.5; DB 4;
; Pred. No. 7.1e-57;
86; Mismatches 193;
                                                                                    518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
                                                                                                                                                                           Sequence 14, Application US/09545814
Patent No. 6416977
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Ctenocephalides felis
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35.8%;
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Best Local Similarity
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EGTVY 511
                                                                                                                                                              US-09-545-814-14
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 559
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A human chitinase, its recombinant production, its use in therapy or prophylaxis against infection diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 IDRAYDIKELNKLFDWMNWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 -EKRGYERFUNLRIKUPELTTMISLGGWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 YINNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
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                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%; Score 738; DB 2; I 34.2%; Pred. No. 4.3e-51; iive 85; Mismatches 150;
                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 11758
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
Sequence 4, Application US/08486839
Patent No. 5928928
GENERAL INFORMATION:
                                                                                                                                                         350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 29,281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 amino acids
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                                                 APPLICANT:
TITLE OF INVENTION: A hu
TITLE OF INVENTION: prof
TITLE OF INVENTION: in t
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                           CITY: Jericho
STATE: New York
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                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                            STREET:
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93 -EKRGYERFNNIRLKNPELITIMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
                                                            325 FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                  --RYPLIQTLRQELSLPYLPSGT 394
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6200951.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
ATITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago STATE: 111inois STATE: 111inois STATE: 111inois STATE: 111inois STATE: 111inois STATE: 10000-6402 SOUTHER: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: FIDOPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOUTHARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/039,198A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.8%; Score 738; DB 3; Lu
34.2%; Pred. No. 4.3e-51;
iive 85; Mismatches 150;
                                                                                                                                                                                                                              445 PSPITPTITPSPITPTTTPS 469
                                                                                                                                                                                                                                                                     395 PELEVP-KPGQPSEPEHGPSPGQDT 418
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Patent No. 6200951
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TELEFAX: (312) 474-6300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amin
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION: INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
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        --RYPLIQTLRQELSLPYLPSGT 394
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Production, Its Use For Decomposing Chitin,
Therapy or Prophylaxis Against Infection Di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
FILING DATE: 10 - September - 1998
ATTORNEY AGENT INFORMATION:
NAME: MOLISS, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECHONE: (516) 822-3550
TELEPHONE: (516) 822-3582
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
                                                                                     445 PSPTTPTTTPSPTTPTTPSPTTPT 469
                                                                                                                             PELEVP-KPGQPSEPEHGPSPGQDT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                  Hoffmann & Baron, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hoffmann & Baron, I
STREET: 6900 Jericho Turnpike
                                                                                                                                                                                                                              Sequence 4, Application US/09151011
Patent No. 6057142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.2<sup>3</sup>
Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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STRANDEDNESS: un
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Syosset
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ZIP: 11791
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          385
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Search completed: March 22, 2004, 07:03:58 Job time : 45.7332 secs

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probable chitinase probable membrane chitinase homolog chitinase chi-A or chitinase - Autogr chitinase - Rutogr chitinase (BC 3.2.

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chitinase (BC 3.2.1.14) [imported] - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 21.Jan.2000 #sequence_revision 21.Jan.2000 #text_change 21.Jan.2000 C;Accession: T44445

R;Shen, Z.; Jacobs-Lorena, M.
Submitted to the EMBL Data Library, June 1997
A;Reference number: Z22771
A;Residues: 1-525 <SHES
A;Residues: 1-525 <SHES
A;Cross-references: EMBL:AF008575; PIDN:AAB87764.1
C;Genetics: A;Genetics: A;Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
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123 FSAWAASGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 PGFISGEEGVLSYIELCOLFOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTT 424
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93; Mismatches 187; Indels
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              T24898
T30418
S47133
A40633
PC4106
T35719
T10393
T10393
T082246
S61166
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G72865
JC4565
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Matches 211; Conservative
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 T44445
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1479.047 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                         March 22, 2004, 06:40:28 ; Search time 36.0951 Seconds
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1 MKTIYAILSIMACIGLMNAS......IMPCPPGTIWCQEKLTCIGE
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                      283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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7114075
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D82510
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Gapop 10.0 , Gapext 0.5
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D83764
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Maximum DB seq length: 200000000
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Match Length DB
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1: pirl:*
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411.5
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Gaps

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411 409.5 408.5 405

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A53918 chitinase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
C;Species: Chelonus sp.
C;Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
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414 APTT----STVAPGTTTTTTTTGANPGTTQPPT--SDAPNHTTTTTTGNPGTTRPPSG 466
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                                                                                                                                                                                                                                                                                                                                                             Chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             937 AGESTRARGFLSYYEICANIRNKKWIYVARDRKGRMGPYAYKGDOWVSFDDOYMIRHKSEY
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                                                                                                                       21 IKRDHNDYSKNPM-----RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
28.0%; Score 869; DB 2; Length 16;
Best Local Similarity 34.3%; Pred. No. 4.8e-46;
Matches 196; Conservative 95; Mismatches 196; Indels
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                                                                                                                                                                                                 536 IMPCPPGTIW 545
                                                                                                                                                                                                                                                       ---CPPGTLF 507
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epidermal and gut
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C;Species: Manduca sexta (tobacco hornworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 NKEAGGGDPAPYTNATGP-----WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AILSIMACIGIMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418) C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U02270; GB:S64757; NID:g406048; PID:g406049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED-
                                                                                                                                                                                                                                                 C,Accession: A56596
R,Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
Insect Biochem. Mol. Biol. 23, 691-701, 1993
A;Title: Sequence of a cDNA and expression of the gene encoding A;Reference number: A56596; MUID:93357793; PMID:8353525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.0%; Score 838.5; DB 2; Best Local Similarity 35.4%; Pred. No. 9.2e-45; Matches 208; Conservative 79; Mismatches 210;
A, Experimental source: larvae
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <KRA>
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A56596
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                               1151
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20;

Gaps

64 55 124 110 183 170 241 230

348

408

WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 343 WVGYEDPRSVEIKANWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS-----FECILGPSITTPITTTPITPIT-----TTPITPS-----PITPITTPSPITTPITTPSP ----SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTAKPASTTKTT

349

409 397 457 450 206

456 449 497

540

-CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC KCYKEGD-IPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC

TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE-------VDGSEI

TIPITIPSPIT------PIP-TIPIPAPIISIPSPITIEHISEIPKYIIYVDGHLI

chitin

us-09-662-293-18.rpr

C;Accession: A53918 R;Krishnan, A; Nair, P.N.; Jones, D. J. Riol Chem 269, 2097-20976, 1994	
A; Title: Isolation, cloning, and characterization of new chitinase stored in active form A; Reference number: A53918; MUID:94342256; PMID:8063715 A; Accession: A53918	OY 96 G-YERPINLRLXNPELTTMISLGGWYEGSEXYSDWAANPTYROOFIOSVLDFLOEYKFDG 154
A.Poscus: preiniminary A.Poscus: 1-483 «KRI» A.Cross-references: GB-110422, NID:9533504, PIDN:AAA61639.1, PID:9533505	OY 155 LDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSPGKDKIDR 207
Chary Match Query Match 25.8%; Score 802; DB 2; Length 483; Best Local Similarity 36.1%; Pred. No. 1.4e-42; Matches 166; Conservative 89; Mismatches 162; Indels 32; Gans 9;	QY 208 AYDIKELMKLEDWMNYMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN 267
4 IVAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCT 62 : : : : :	Qy 268 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK 327 288 KGWPKEKIIVGMPTYGRGWTLNNASAINPGTSGSPAKITQYVQ-EAGVGAYFEFCEMLAN 346
Oy 63 HIMYGPAKIDEYKYTIQVPDPYQDDNHNSWEKRGYERFNNIRLKNPELITWISLGGWYEG 122	CY 328 EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVAVWSLENDDFKGHC 387 DD 347 GATR-YWDSQSQVPYLVQGNQWMSYDDEBSPANKWAYVKREGYGGAFVWTLDFDDFNAGC 405
	Qy 388 GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTP 429 Db 406 SNSNGQLYPLISVIAKELGGVIIPKKGGVTTAPTTVATTVTTGRPPMTSAVTT 458
OY 183 LKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMYWTYDYHGGWENFYG-HNAP 241	Qy 430 TTTPTTPSPTTTPSPTT
LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAK	CY 450PITIPSPITPITEPSPITPITPIPAPITSTPSPITTEHISETPKYTTVDGH 503
GMSPPGFISGEEGVLSYIELCQLFQKGEWHIQYDBYYNAPYGYNDKIWVGYDDLASISCK 34	Qy 504 LIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIMCQEKL/TC 552
OY 362 LAFLKELGVSGVMVWSLENDDFKGHCGPRNPLLNKVHNMINGDEKNSFECILGPSTT 418	RESULT 6 S57197 oviduct-specific glycoprotein 95K precursor - bovine (fragment)
OY 419 TPTTTTTTTTTTPTTPSPTTP 441	C,Species: Bos primigenius taurus (cattle) C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999 C;Accession: S57197 R:Sendai, Y:, Abe, H.; Kikuchi, M.; Satoh, T.; Hoshi, H.
RESULT 5 T15408	bovine :81992
hypothetical protein CO4F6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15408	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-537 <sen> A;Cross-references: EMBL:D16639; NID:g391621; PIDN:BAA04065.1; PID:d1004583; PID:g39162</sen>
Alloward to the EMBL Data Library, December 1995 Albescription: The sequence of C. elegans cosmid C04F6. AlReference number: 218346 AlAccession: T15408	Cineywords: glycopiocein Query Match Best Local Similarity 33.3%; Pred. No. 3e-35; Matches 173; Conservative 95; Mismatches 183; Indels 69; Gaps 19;
A;Scatus: preliminary; translated from GH/EMBL/DDBJ A;Wolecule type: DNA A;Residues: 1-617 <nha> A;Cross-references: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CESP:CO4F6</nha>	Qy 10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYIIEDIDPFKCTHLMYG 67 :: : : : : : : :::
Cjenetics: AjGene: CESP;CO4F6.3 AjIntrons: 28/1; 66/2; 504/1	68 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS
Query Match 22.7%; Score 705.5; DB 2; Length 617; Best Local Similarity 30.2%; Pred. No. 2e-36; Matches 178; Conservative 90; Mismatches 210; Indels 111; Gaps 19; Qy 37 CYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKR 95	DB SS FASMSNNQIVPKDF-QDEKILYPEFNKLKERNRGLKTLLSIGGWNFGTVKFT 105 QY 128 DMAANPTYRQQFIQSVLDFLQBYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187 Db 106 TMLSTFSNRERFVSSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWFFVFLLEELLQAF 164

Qy 419 TPTPTTTPTTPTTPTTPSPTTPTTPSPTTPTTTPSPTTPTTPSPT 466 Db 390 TPSPKFWFSTAVNSSRIGPBMPTMTRDLTTGLGILPLGGEAVATETHRKSATMTTTPRGE 449 Qy 467 TPTPT-TPTPAPTTSTPSPTTEHTS 491 Db 450 TATPTTTPLSSGRRTAAPEGKTESPGEKDLTS 481 RESULT 8 138605 Oviductal glycoprotein - human C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;5pecies: Homo sapiens (man) C;bate: 29-May-1998 #fext_change 29-May-1998 C;Accession: 138605 R;Arias, E.B.; Verhage, H.G.; Jaffe, R.C. Biol. Reprod. 51, 685-694, 1994 A;Aties: Complementary deoxyribonucleic acid cloning and molecular characterization of a A;Reference number: 138605; MUD:95119256; PMID:7819450 A;Redremce number: 138605; MUD:95119256; PMID:7819450 A;Redremce number: 118605 A;Residues: 11684 KRES- A;Molecule type: mRNA A;Residues: L-654 KRES- A;Coss = 1-654 KRES- A;Coss	OCTE 668; ed. No. 4. Mismatche PMRINCYVGT FILL KLVCYFTN NSWEKRGYER NSWEKRGYER NSWEKGLDLDW EKILYPE DXIDRAYDIR STATOGLDLDW STATOGLDLDW STATOGLDLDW STATOGLDLDW STATOGLDLDW STATOGLDLDW		Oy 359 SCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KNPLLNKVHNMINGDEKNSFECILGPS 416 Db 338 SYKAWFIRREHFGGANVWTLDMDDVRGTFCGTGPFPLVYVLNDILVRAEFSS 389 Qy 417 TTTPTPTTTPTTPTTPTTPSPTTPTTPSPTTPTTPSPTTPTTTPSPT 466	Db 450 TVTPTKETVSLGKHTVALGEKTEITGAMTMTSVGHQSMTPGEKALTPV-GH 499 RESULT 9 A49562 cartilage glycoprotein gp39 precursor - human N,Alternate names: 39K synovial protein C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 22-Jun-1999
OY 188 EPHGYILITAAVSPGKDKIDRAYDIKELMKLEDWMAVATYDYHGGWENFYGHNA 240 165 KNEAQLIMEPRILLSAAVSGDPHVVQKAYEARLIGRILDFISVLSYDLHGSWEKVIGHNS 224 OY 241 PLYKRPDETDELHTYFWNYTMHYYLMNGATRDKLWGVPFYGRAWSIEDRSKLKLGDPA 300 225 PLESLPGDPKSSAYAMNYWRQLGVPPEKLLMGLPTYGRTFHLLKASQNELRAQA 278 OY 301 KGMSPPGFISGEECVLSYIELCQLFQKBEWHIQYDEYYNAPYGYNDLASISC 360 10	dependent oviduct protein precursor - sheep 5-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999 1. 146470 A.M. Murzay, M.K. 1. Marzay, M.K. 2. Marzay, M.K. 3. Marzay, M.K. 4. Marzay, M.K.	ASIKRDHNDY SIKRDHNDYLMLKHHDG TIQVFDPYQD	QY 128 DWAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALUNELKDAF 187 Db 109 KMLSTFSNRERFVKSVIALLRTHGFDGLDLFFLYPGLR -GSPARDRWTFVFLLEBILQAF 167 QY 188 EPHGYLLTAAVSPGKDKIDRAYDIKELNKIFDWMYNTYDYHGGWENFYGHNA 240 Db 168 KNBAQLTMRPRLLLSAAVSGDPHVIQKAYDARLLGRLLGFISVLSYDLHGSWEKVTGHNS 227 QY 241 PLXKRPDETDELHTYFNVNYTWHYYLMNGARDLVMGVPFYGRAWSIEDRSKLKLGDPB 300 QY 241 PLXKRPDETDELHTYFNVNYTWHYYLMNGARDLVMGVPFYGRAWSIEDRSKLKLGDPB 300	Db 228 PLFSLPGDPKSSAYAMSYWRQLGVPPEKLLMGLPTYGRTFHLLRASQNELGAGA 281 Qy 301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

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                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 GPDGLDLAWISPGRR-----DKRHLTTLVKEMKARFVREALPGTERLLLSGAVSAGKVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 VLRLGAPANKLVMGIPFFGRSFTLAS-SKTDVGAPASGPGIFGRFTKEKGILAYYELCDF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAPLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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A Status: nucleic acid sequence not shown
A Molecule type: mRMA
A; Residues: 1-405 < AMOR1>
A; Cross-references: EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; PID:g1085066
R; Morrison, B.W.
Submitted to the EMBL Data Library, November 1995
A; Reference number: 861550
A; Rocession: 861550
A; Molecule type: mRNA
A; Residues: 1-245, '1', 247-330, 'H', 332-350, 'MWMALDLDDFQGTCQPKEFFPLTNAIKDALA' < A; Cross-references: EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; PID:g1085066
A; Note: the differences at the carboxyl end are due to a frameshift error
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #text_change 20-Jun-2000
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C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-405/Product: breast-regressing protein brp39 #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_
C;Accession: 861551; 861550; 148271
R;Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A;Teile: neu and ras initiate murine mammary tumors that A;Teile: neu and ras initiate murine mammary tumors that A;Reference number: 148271; MUID:95060797; PMID:7970700
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                     ed. No. 3.1e-33;
Mismatches 130;
                     Pred. No.
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GNFCGONLRFPLTSAIKDVL 380
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                     Best Loca
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       C;Accession: A49562; S10677; A33162

R;Hakala, B.E.; White, C.; Recklies, A.D.
U. Biol. Chem. 268, 25803-25810, 1993

A;Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and A;Reference number: A49562; MUID:94064658; PMID:8245017

A;Rectus: preliminary

A;Molecule type: mRNA

A;Residues: 1-38 x-HAX.

A;Residues: 25-40; Will:90328983; PMID:2375755

A;Recture number: S10677; MUID:90328983; PMID:2375755

A;Roccule type: protein

A;Residues: 22-40; X', 42-45 x-NY2.

C;Superfamily: Streptomyces chitinase chi40

C;Superfamily: Streptomyces chitinase chi40

C;Superfamily: Streptomyces chi40

C;
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21.3%; Score 662; DB 2; Length 38
Best Local Similarity 34.9%; Pred. No. 5.5e-34;
Matches 144; Conservative 81; Mismatches 136; Indels
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CiDate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_CiDate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_CiDate: 55132.
CiDate: 10-Mar Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
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A; Accession: S51327
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Length 383;

7

В

Score 650;

20.9%;

Match

Query

brugian

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C;Species: Brugia malayi
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A3221
F;Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A;Title: Transmission-blocking antibodies recognize microfilarial chitinase
A;Reference number: A38221; MUID:92179220; PMID:1542646
            (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
Brugia malayi
                                                                                                                                                                                                         A; Residues: 1-504 <FUH>
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                                                                                                                                                           324 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGV----MVWSLE 379
                                                                                                                                                                                                                                          303 FLKGABVHRLSNE--KVPFATKGNOWVGYEDKESVKNKVGFLKEKKLAGAWCGHWIWMI- 359
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                                                                  KIDRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTWH 263
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house revision 17-Apr-1993 #text_change 22-Jun-1999
Cidacession: $27879
Richang, N.C.A.; Liu, C.H.; Chang, A.C.
Submitted to the ENBL Data Library, June 1992
A; Description: Molecular characterization of a secretory protein (YM-1) tran A; Reference number: $27879
A; Accession: $27879
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mBNA
A; Molecule type: mBNA
Cross_references: EMBL:M94584; NID:g202441; PIDN:AAB62394.1; PID:g202442
C; Superfamily: Streptomyces chitinase chi40
C; Superfamily: stgmal sequence #status predicted <SIG>F; 22-399/Product: secretory protein YM-1 #status predicted <MAT>
                     185 AIDTGYDIAQIAQHLDFINLMTYDFHGVWRQITGHHSPLFQGQCDT-RFDRYSNVNYAVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKI--DEYKYTIQVFDPYQDDNHN
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Best Local Similarity 36.3%; Pred. No. 1.3e-30;
Matches 141; Conservative 67; Mismatches 140; Indels
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13

RESULT

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A;Status: preliminary
Modecule Lype: DNA
A;Residues: 1-599 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04635.1; GSPDB:GN00
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C;Species: Bacillus halodurans
C;Species: Dac-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83764
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Réference number: A83650; MUID:20512582; PMID:11058132
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                                                                                                                                                                                                                                                                                                                                   37 CYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQ-DDNHNSWEK
                                                                                         A;Cross-references: GB:M73689; NID:g156063; PIDN:AAA27854.1; PID:g156064
A;Note: sequence extracted from NCBI backbone (NCBIP:85345)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                            69;
A, Status: preliminary, not compared with conceptual translation A, Molecule type: nucleic acid; protein
                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                           Query Match
19.5%; Score 604.5; DB 2;
Best Local Similarity 30.1%; Pred. No. 3e-30;
Matches 156; Conservative 86; Mismatches 208;
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23;

Gaps

156;

Indels

67; Mismatches 185;

102

71

117

162

173

221 227 280 283 339

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RAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQXEEWHIQ---YDEYYN- 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---APYGYN--DKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 NKVHNMINGDEKNSFECILGPSTTTPTPTTTTTTTTTTPTTTP-----------436
                                                                                                                                                                                                GWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYP--GSRLGNPK--1DK
                                                                                                                                                                                                                                                                                                                                                                                                        KIVGYYPSWAAYGR--NYNVADIDPTKVTHINYAFADICWNGIHGNPDPSGPNPVTWTCQ
                                                                                                                                                               DEYKYTIQV-----FDPYQDDNH----NSWEK---RGYERFNNLRLKNPELTTMISLG
                                                                                                                                                                                                                                                                                                                       GW-TWSNRFSDVAATAATREVFANSAVDFLRKYNFDGVDLDWEYPVSGGLDGNSKRPEDK
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                                                   34 RIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKI-
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 TPEHFNVESAVEGHLQAGVPEHKLVLGMPFYGRGWSNCDGA--NQGEYQR-CAPPREGTW 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 LQEYKFDGLDLDWEYP--GSRLGNPK--IDKQNYLALVRELKDAFEPHG-----YLLITA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 A--VSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETD-ELH 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T--YFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISG 311
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                                                                                                                                                                                                             2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKC
                                                                                                                                                                                                                                                                                                                    THLMYGRAK-----DNP
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                                                                                                                                                               Gaps
                                                                                                    19.1%; Score 592; DB 2; Length 599;
29.0%; Pred. No. 2.3e-29;
ive 98; Mismatches 216; Indels 134;
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A, Experimental source: strain C-125 C, Genetics:
A, Gene: BH0916
                                                                                                      Query Match
Best Local Similarity 29.0%
Matches 183; Conservative
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completed: March 22, 2004, 07:01:30 e : 38.0951 secs
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Score 561; DB 2; Length 699; Pred. No. 2.3e-27;

18.1%; 29.4%;

Query Match Best Local Similarity

546

-----PSPTT 458

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us-09-662-293-18.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 22, 2004, 06:31:13; Search time 21.2868 Seconds (without alignments) 1357.597 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-662-293-18 3107 1 MKTIYAILSIMACIGLMNAS......IMPCPPGTIWCQEKLTCIGE 555

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descr	P36362 manduca sex	homo sap	O91xa9 mus musculu	dros	homor			bos tauru	ovis	mus n	mes	Q62010 mus musculu	ношо	homod	papic	homo	mus m	_	drosop	P20533 bacillus ci	trichoder	-	α	P32823 alteromonas	0			60	P54196 coccidioide	0	156	19275	02817
SUMMARIES		CHIT MANSE	CHT1 HUMAN	CHIA_MOUSE	CHI1_DROME	CHIA_HUMAN		OGP_FIG	OGP_BOVIN	OGP_SHEEP	C3L1_MOUSE	OGP MESAU	OGP MOUSE		C3L1 HUMAN	OGP PAPAN	C3L2_HUMAN	CHT1 MOUSE	CHIT_BRUMA	CHI3_DROME	CHI1_BACCI	CHI4_TRIHA	CHI1_APHAL	CHIA_SERMA	CHIA_ALTSO	CHIT_NPVOP		CHIB SERMA		CHI1_COCPO	CHIT STRPL	CHID VIBFU	VTP3 TTV1V	MUC2_HUMAN
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Q62635 rattus norv Q05049 xenopus lae Q10341 orgyia pseu P1067 xenopus lae P22533 caldocellum P14918 zea mays (m Q06885 dictyosteli P47179 saccharomyc P22699 dictyosteli P09805 kluyveromyc P24152 sorghum bic P02840 drosophila
MUC2_RAT MUC1_XENLA X091_NPVOP MANB_CALSA EXTN_MAIZE GP10_DICDI DN44_YEAST GWG_DICDI KTXA_KLULA KTXA_KLULA KTXA_KLULA
1513 662 279 279 1331 267 1161 705 1163 307
00000000000000000000000000000000000000
244 244 238 230 227.5 221 2217.5 2117.5 2115.5 208.5
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ALIGNMENTS

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND SUBCELLULAR
                                                                                                                                                                                                                 SEQUENCE OF 22-42 AND 178-198, FUNCTION, AND TISSUE SPECIFICITY MEDLINE=95138187; PubMed=7836450;
                                                                                                                                   Boot R.G., Renkema G.H., Strijland A., van Zonneveld A.J., Aerts J.M.F.G.;
"Cloning of a CDNA encoding chitotriosidase, a human chitinase produced by macrophages.";
J. Biol. Chem. 270:26252-26256 (1995).
                                                                                                                                                                                                                                        Renkema G.H., Boot R.G., Muijsers A.O., Donker-Koopman W.E., Aerts J.M.F.G.,
"Furification and characterization of human chitotriosidase,
member of the chitinase family of proteins.",
J. Biol. Chem. 270:2198-2202(1995)
                                                                                                                                                                                                                                                                                                                                                   Boot R.G., Renkema G.H., Verhoek M., Strijland A., Bliek J., de Meulemeester T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G. "The human chitotriosidase gene. Nature of inherited enzyme deficiency.";
                                                                                                                                                                                                                                                                                                                            POLYMORPHISM, AND DESCRIPTION OF ISOFORM 3.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=98421482; PubMed=9748235;
                                                                                                          TISSUE=Macrophage;
MEDLINE=96064695; PubMed=7592832;
                sapiens (Human)
                                                        NCBI_TaxID=9606;
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  SE IYSFIGVTEGNSEVLIIDPELD----VDKNGFRNFTSLRSSHPSVKFWVAVGGWAEGSS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 WYGYEDPRSVEIKANWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS----- 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
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Pfam; PF001607; CBM_14; 1.
Pfam; PF00704; GlyCo_hydro_18; 1.
ProDom; PD000471; GlyCo_hydro_18; 1.
SMART; SM00494; ChEBD2; 1.
SMART; SK00636; GlyCo_18; 1.
SMART; SK00636; GlyCo_18; 1.
PROSITE; PS50940; CHIT_BINIA, 1.
PROSITE; PS00195; CHITIBINIA, 18; 1.
PROSITE; PS01963; CHITIBINIA, 18; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                  SER/THA-RICH.
CHITIN-BINDING TYPE-2.
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                   91;
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                                                                                                                                                                                                                                                                          DB 1; Length 554;
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                                                                                                                                                                                                                                                                        ; Score 838.5; DB 1; Length E; Pred. No. 6.3e-39; 79; Mismatches 210; Indels
                                                                                                                                                                                                                                               3989D756C96CD490 CRC64;
                                                                                                                                       ENDOCHITINASE
                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                               62203 MW;
                                                                                                                                                                                                                                                                        27.0%;
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Best Local Similarity 35.4
Matches 208; Conservative
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396
4495
146
303
407
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novel

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Isold=Q13231-3; Sequence=VSP 008633;
Note=Duplication of 24 bp in exon 10 leads to the use of a
cryptic splice site. The normal splice site is still present but
                                                                                                                                                                                   Fusetti F., von Moeller H., Houston D., Rozeboom H.J., Dijkstra B.W., Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;

Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;

"Structure of human ohitotriosidase. Implications for specific inhibitor design and function of mammalian chitinase-like lectins.";

J. Biol. Chem. 277:25537-25544(2002).

-! FUNCTION: Degrades chitin and chitotriose. May participate in the argumatic activity.

-! CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophages.

POLYMORPHISM: A 24 bp duplication in exon 10 leads to the activation of an alternative splice site and the production of an inactive protein. About 6% of the population are deficient for CHITI activity, while 35% are carriers and show reduced enzyme levels. People with CHITI deficiency appear perfectly healthy. MISCELLANBOUS: Patients with type I Gaucher disease (GD I) [MIM.230800] have very high plasma levels of CHITI, and this can be used as diagnostic aid and to evaluate the success of treatment. Successful therapy brings the CHITI activity levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBGELLUAR LOCATION: Secreted. A small proportion is lysosomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Detected in spleen. Secreted by cultured
                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-386 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of acetyl-D-glucosamine polymers of chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_008632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q13231-2; Sequence=VSP_008631,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q13231-1; Sequence=Displayed;
J. Biol. Chem. 273:25680-25685(1998)
                                                                                                                      CHITOBIOSE AND ALLOSAMIDIN.
MEDLINE=22095530; PubMed=11960986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          back to normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=3
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CHT1 HUMAN STANDARD, PRT; 466 AA. 013231; Q9H3V8; L15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Chitotriosidase 1 precursor (EC 3.2.1.14) (Chitinase 1).

RESULT 2
CHT1 HUMAN
ID CHT1 HT
OC 013231
DT 15-MAR
DT 15-MAR
DT 15-MAR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 -EKRGYERFUNLALKUPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 IDRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTWHY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGPISGEEGVLSYIELCQL 324
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                                                                                                                                                                                                                                                                                                          And GO: 000515; C:extracellular space; TAS.

R GO: GO: 000558; F:chitinase activity; TAS.

R GO: GO: 0005615; P:response to bacteria; TAS.

R GO: GO: 000513; P:response to bacteria; TAS.

R GO: GO: 000513; P:response to bacteria; TAS.

R GO: GO: 000557; Chitin_bind_PerA.

InterPro: IPR001223; Glyco_hydro_18.

InterPro: IPR001579; Glyco_hydro_18.

R Pfam; PF00704; Glyco_hydro_18.

R Pfam; PF00704; Glyco_hydro_18; 1.

R ProDom; P0000471; Glyco_hydro_18; 1.

R MART; SM00494; ChtBD2; 1.

R RMART; SM00494; ChtBD2; 1.

R RNSITE; PS001095; CHTTNASE 18; 1.

R PROSITE; PS01095; CHTTNASE 18; 1.

R PROSITE; PS01095; CHTTNASE 18; 1.

R POLYSACCharide degradation; Hydrolase; Glycosidase; Chitin-binding; Simple of the contains of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.8%; Score 738; DB 1; Length 466; ilarity 34.2%; Pred. No. 1.6e-33; Conservative 85; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SL -> NG (in isoform 2).
/FTIG=VSP 008631.
Missing (In isoform 2).
/FTIG=VSP 008632.
Missing (In isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId~VSP 008633.
51681 MW; B4312D1E885E386D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHITOTRIOSIDASE 1.
CHITIN-BINDING TYPE-2.
BY SIMILARITY.

    Signal, Alternative splicing, 3D-structure.

    SIGNAL

    1

    21

    CHITOTRIOSIDASE

    CHAIN

    ACT

    ACT

    SITE

    140

    BY

    SIMILARITY.

    DISCULPID

    307

    VARSPLIC

    386

    387

    SL -> NG (in is

                                                                                                                                                               EMBL; U29615; AAC50246.1; -.
EMBL; U62662; AAG10644.1; -.
PDB; 1GUV; 31-JAN-02.
                                                                                                                                                                                                 PDB; 1GUV; 31-JAN-02.
PDB; 1LG1; 18-SEP-02.
PDB; 1LG2; 18-SEP-02.
PDB; 1LQ0; 29-UUL-03.
Genew; HGNC:1936; CHITI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
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es 152; Conserv
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Matches
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STRAIN-C57BL/6J; TISSUE-Stomach;

RADINE-2108S660; DubMed-11217851;

MEDLINE-2108S660; DubMed-11217851;

RADINE-2108S660; TARSUE-Stomach;

RADINE-2108S660; TARSUE-Stomach;

RADINE-2108S660; TARSUE-Stomach;

RADINE-2108S660; TARSUE R., Stone H., Adachi J., Fukuda S.,

RADINE-2108S660; T., Stunni T., Bono H., Radukawa T., Saito R.,

RADIO T., Okazaki Y., Gojobori T., Sano H., Raukawa T., Saito R.,

RADIO T., Okazaki Y., Ashburner M., Batalov S., Casavant T.,

RADIO T., Masted H., Ashburner M., Batalov S., Casavant T.,

RADIO T., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RADINE-210, Boffelli D., Bojunga N., Azminci P., de Bonaldo M.,

ROMINIO P., Marchionni L., Mashima J., Mazzarelli R., Barsh G.,

ROGONE P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hyashizaki Y., Poshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayshizaki Y., Poshida K., Hasegawa Y., Kawaji H.,

RADIO P., Marchioni L., Mang K.H., Weitz C., Whittaker C., Wilming L.,

RADIO P., Washizaki Y., Kawaji H., Kohtsuki S.,

RADIO P., Kawaji Y., Yayo-Aka Y., Wangi Y., Yayo-Aka Y., Wangi Y., Kawaji Y., Kawaji Y., Yayo-Aka Y., Wangi Y.
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Mcguan D.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                     GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21125893; PubMed=11085997;
Boot R.G., Blommaart E.F.C., Swart E., Ghauharali-van der Vlugt K.,
Bijl N., Moe C., Place A., Aerts J.M.F.G.;
"Identification of a novel acidic mammalian chitinase distinct from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIA MOUSE STANDARD; PRT; 473 AA.
Q91XA9; Q99PH2; Q9D803; Q9JLN1;
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase) (YNL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MusinCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 22-43, TISSUE SPECIFICITY, AND FUNCTION.
                                                                                                                                                                                                                                                                             -- FSCNOG-
                                                                                                                                                                                                                                                                                                                                                                                      PSPTTPTTTPSPTTPSPTTPT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 PELEVP-KPGQPSEPEHGPSPGQDT 418
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J. Biol. Chem. 276:6770-6778(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE=Lung;
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Fouchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                        ACIDIC MAMMALIAN CHITINASE.
CHITIN-BINDING TYPE-2.
BY SIMILARITY.
BY SIMILARITY.
P -> A (IN REF. 1).
P -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                hydrolases).
SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004568; F:chitinase activity; IDA. GO; GO:0006032; P:chitin catabolism; IDA. InterPro; IPR002557; Chitin bind PerA. InterPro; IPR001223; Glyco hydro 18. InterPro; IPR001579; Glyco hydro 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AKOO8633) BAB25795.1;
EMBL: BCO1134; AAH11134.1; ALT_INIT.
EMBL: BCO34548 AAH34548 1; ALT_INIT.
EMBL; AF154571; AAF31644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF290003; AAG60018.1; -.
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                                                                                                                                     SEQUENCE OF 2-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1932052; Chia.
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473 AA;
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DISULFID
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SIGNAL
CHAIN
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                       191
                                                                                                                                                                                                                                                233 TETGS-NAYLNVDYVWNYWXNNGAPAEKLIVGFPEYGHTFILRNPSDNGIGAPTSGDGPA 291
                                                                                                                                                                                                                                                                                                                          292 GPYTRQAGFWAYYEICTFLRSGATEVW----DASQEVPYAYKANEWLGYDNIKSFSVKAQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                     392
75 KYTIQVFDPYQDDNHNSW-EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANP 133
                                                                                                            114 ONRÓTFITSVIKFLRQYGFDGLDLDWBYPGSR-GSPPQDKHLFTVLVKEMREAFEQEAIE 172
                                                                                                                                                                                                                                                                                                     GFISGEEGVLSYIELCQLFQK---ESWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLA 363
                                                                                                                                                                                                                           DETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPP
                                                                       134 TYRQOFIOSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG--
                                                                                                                                                                                    173 SNRPRLMVTAAVAGGISNIQAGYEIPELSKYLDFIHVMTYDLHGSWEGYTGENSPLYKYP
                                                                                                                                                                                                                                                                                                                                                                                                                   348 WLKONNFGGAMIWAIDLDDFTGSFCDOGKFPLTSTLNKA------LGISTE
                                                                                                                                                 192 ----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRP
                                                                                                                                                                                                                                                                                                                                                                                364 FLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
"Chtrinases are a multi-gene family in Aedes, Anopheles and
Droschila.";
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
Yasuhara J.C., Wakimoto B.T., Myers B.W., Celniker S.B., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heterochromatic sequences in a Drosophila whole-genome shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Canton-S;
MEDLINE=98324849; PubMed=9662472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 151-263 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 TPTPTTFTTF 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 GCTAPDVPSEPVTTP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly.";
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57;

DB 1; Length 473;

23.6%; Score 734.5; DB 1; Length 36.3%; Pred. No. 2.5e-33; tive 72; Mismatches 148; Indels

Matches 158; Conservative

13

ð g

Similarity

Local

Query Match

16 LANASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEY LLNAQLGSAYN-----LICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNN

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chitotriosidase.
      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 EYNFDGLDLDWEYPVCWQVDCKKGTAE-EKIGFSALVRELFYAFQPRGLILSAAVSPNKK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 VIDAGYEVAELSHYFSWISVMAYDYHGQWDKKTGHVAPMYSHPEGT----ANFNANFSWN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 LFQKEEWHIQYDEYYN-APYGYNDKIWYGYDDLASISCKLAFLKELGVSGVMVWSLENDD 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 323
                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                 34 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDBYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EKRGYERFINILRLKNPELTTMISLGGWYEGS-EKYSDMAANPTYRQOFIOSVLDFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 EYKFDGLDLDWEYP----GSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSPGKD
                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
TISSUE=Lung, and Stomach;
MEDLINE=21125893; Pubmed=11085997;
                                                          FlyBase, FBgn0022703; Cht1.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR00123; Glyco_hydro_18.
InterPro; IPR001270; Glyco_hydro_184.
Prof0004; Glyco_hydro_18; 2.
ProDom; PD000471; Glyco_hydro_18; 2.
PROSITE; PS01095; CHTINASE 18; 1.
PROSITE; PS01095; CHTINASE 18; 1.
ACT_SITE 264 264 PROTON DONOR (BY SIMILARITY).
SEQÜENCE 508 AA; 57751 MW; 26CA23B02EFDEB97 CRC64;
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SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
MEDLINE=20018184; PubMed=10548734;
Saito A., Ozaki K., Fujiwara T., Nakamura Y., Tanigami A.;
"Isolation and mapping of a human lung-specific gene, TSA1902, encoding a novel chitinase family member.";
Gene 239:325-331 (1999).
                                                                                                                                                                                                                                                                                             Query Match 23.3%; Score 723; DB 1; Length 508; Best Local Similarity 39.8%; Pred. No. 1.1e-32; Matches 144; Conservative 71; Mismatches 121; Indels ;
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OSBZP6; O86UD8; Q9ULY4;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase)
    send an email to license@isb-sib.ch)
                                    EMBL; AF026500; AAB81858.1; -.
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B BOOR R G., Blommaart E.F., Swart B. Chantarali-van der Vlugt K., Blin, Noe C., Blace A., Aerts J.M.P.G.;

"Identification of a nowal acidic mammalian chitinase distinct from the international of a nowal acidic mammalian chitinase distinct from a transfer gar. 276-6770-6730(201).

RESTERCATION OF A NOWALLAY 1932,

RESTRICTED OF A NOWALLAY 1932,

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MEDLINE=98324849; PubMed=9662472;
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 -EKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLQEYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDGLDFDWEYPGSR-GSPPQDKHLFTVLVQEMREAFEQEAKQINKPRLMVTAAVAAGISN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEGVLSYIELCQL 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDVTLYQAFNGLKNKNSQLKTILLAIGGWNFGTAPFTAMVSTPENRÓTFITSVIKFLRQYE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
PROSITE; PS50940; CHIT BIND II; 1.
PROSITE; PS01095; CHITINASE 18; 1.
Carbohydrate metabolism; Chitin degradation;
Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding; Signal; Alternative splicing. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 476;
                                                                                                                        BY SIMILARITY.
ACIDIC MAMMALIAN CHITINASE.
CHITIN-BINDING TYPE-2.
POLY-SER.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSING (In isoform 3).
/FIId=VSP_008634.
MISSING (In isoform 2).
MISSING (In isoform 2).
IT=Y (IN REF. 1).
V -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 708.5; DB 1; Length 4; Pred. No. 6.4e-32; 75; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases.
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01-NOV-1997 (Rel. 35, Last sequence update)
115-MR-2004 (Rel. 43, Last annotation update)
175-MB-2004 (Rel. 43, Last annotation update)
CHT-1 OR CO4F6.3
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Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                 52271 MW;
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35.9%;
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432 4
476 AA;
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Q11174; 017321;
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CONFLICT
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DOMAIN
ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 GYDIPNLAPNFDFILLMSYDFFGAWASLVGFNSPLYATTELPAEWNGW-NVDSSARYWNQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 KGMPKEXIIVGMPIYGRGWILINNASAINPGISGSPAKIIQYVQ-EAGVGAYFEFCEMLAN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 AYDIKELNKLPDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PTTTPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 G-YERFINILRLKUPELTIMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 GATR-YWDSQSQVPYLVQGNQWWSYDDEESFANKMAYVKREGYGGAFVWTLDFDDFNAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111; Gaps
                                                                               Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ycosidas; Chitin degradation; Chitin-binding; Repeat. 178 534 CHITIN-BINDING TYPE-2 1. CHITIN-BINDING TYPE-2 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 617;
Robbins P.W.;
in Aedes, Anopheles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 2 chitin-binding type-2 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W -> C (IN REF. 2).

ITF -> TTS (IN REF. 2).

I -> L (IN REF. 2).

DDA1D2AAACOE54DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 705.5; DB
Pred. No. 1.3e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mormbep, C04F6.3; CE03923.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18.
Efam; PP01004; Glyco_hydro_1845.
Pfam; PP00104; Glyco_hydro_18; 1.
ProDom; P000047; Glyco_hydro_18; 1.
ProDom; P000047; Glyco_hydro_18; 1.
ProDom; P000047; Glyco_hydro_18; 1.
PROSITE; PS01095; GHYC_BIND_II; 2.
PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THR-RICH.
   le la Vega H., Specht C.A., Liu Y.,
'Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.7%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U42835; AAA83586.1; -.
EMBL; AF026152; AAB81847.1; -
PIR; T15408; T15408.
PIR; T37249; T37249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.29
Marches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617 AA;
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LILWVGLV--LVLKHHNGAAH----KLVCYFANWA-FSRPGPASILPRDLDPFLCTHLVFA

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                                                                                                     503
                                                                                                                                   564
----PTTTPSPTTPSTTTPSPTTPTPTPTPAPTTSTPSPTTTSHTSETPXTTYVDGH
                                                                                                                     459 İTAATTITTRAATTITTASNTNVCSGKSDGFYPNSNNCGLFVLCLSSKSYSMSCPSGLQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITPITPSPITPITTPSPIT-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%; Score 696.5; DB 1; Length 527; 34.6%; Pred. No. 3.2e-31; ive 86; Mismatches 192; Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (POSP-E3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OVIDIOT-SPECIFIC GLYCOPROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                             LIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
                                                                                                                                                                              --KCIXDGFFGVPSDCLKFIRC--VNG--ISYNFECPNGLSFHADIWMC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: Oviduct. -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKED (GLCNAC. . .) (P. 31B78F49CA2363A2 CRC64;
                                                                                                                                                                                                                                                                     527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
Prom; PR001679; Glyco hydro 18; I.
SMART; SM00636; Glyco hydro 18; I.
PROSITE; PS01095; Glyco 18; I.
PROSITE; PS01095; Glyco 18; I.
21 Glycoprotein; Fertilization; Signal.
21 Glycoprotein; Fertilization; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58519 MW;
          406 SNSNGQLYPLISVIAKELGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U43490; AAA85445.1; -.
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            OVGP1 OR OGP.
                                         430
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SEQUENCE
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                                                                                                                                                                                                                                                                   OGP_PIG
Q28990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                           227
                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                           358
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                     58 FASANDSQIVAK-----DARD--ESIFYPEFNQLKERNEKLKTLLSIGGWNFGTSRFT 108
                                                                                                                 167
                                                                                                                                                      240
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                                                                                                                                                                                                                                                                                                                                                                                   SCKLAFLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECIL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSTTVNSSRTCPESLAVTKDLTTDLGILPLGGEAVATETHGRSDNM-TVTPGGGGLVAPT 454
                                                                                                 109 TWLSTFTWREKFIRSAIGLIRTHGFDGLDLFFLYPGLR-GSPRADRWNFLFLLEELLLAF
                                                                                                                                                                          241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                                                                                                                                                                                                                            282 VGPASPGKYTKQAGFLAYYEVCSFVQRAKKRW---IDHQY-VPYAYRGKEWVGYDDDISF
                                                                                                                                                                                                                                                                                                                                                                                                         338 SYXAFFIKKEHFGGAMVWTLDLDDVRGTFCGTGPPFLVYMLNDL--LLKAEVSSTLSPGF
 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS
                                                                          128 DMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF
                                                                                                                                                    EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                                PLFSLSDDPK-----SSAYTMNYWRKLGAPPEKLLMGFPTYGRTFRLLKASKNELGAEA
                                                                                                                                                                                                                                                                                                         KGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASI
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Biol. Reprod. 50:927-934(1994).
-!- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role
in the fertilization process and/or early embryonic development.
-!- SUBCELLULAR LOCATION: Secretory granules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
001-NOV-1997 (Rel. 35, Last annotation update)
001-NOV-1997 (Rel. 35, Last annotation update)
001-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 19-47.
TISSUB-Oviduct;
MEDLINE=94257768; PubMed=8199272;
Sendal Y., Abe H., Kikuchi M., Satch T., Hoshi H.;
"Purification and molecular cloning of bovine oviduct-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: Oviduct.
-i- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPTLSFGKLTVÁÞEGKTESÞGEKAMTPVGHPSVTP 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 TP-----TPAPTTSTPSP----TTTEHTSETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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Q28042;
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 68
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OGP_BOVIN
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Conservative

Local Similarity

Best Local Simi Matches 178;

19;

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development.
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                     241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                                                                                                                                                                                                                                                                                                                                                               301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                                                                                                                                                                                                                                                                                                                                                                                279 VGPASPGKYTKQAGFLAYYEICCFVRRAKKRWINDQY--VPYAFKGKEWVGYDDAISFGY 336
                                                                                                                                                                                                                                                                                                                                                                                                   KLAFLKELGVSGVMVWSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                        387 TPSPKFWFSTAVNSSRIGPEMPTMTRDLTTGLGILPPGGEAVATETHRKSETMTITPKGE 446
                                                                                                                                                                                                                                              DMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF 187
                                                                                                                                                                                                                                                                                               68 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELITMISLGGWYEGSEKYS 127
                                                                                                                                                                                       54
                                                                                                                                                                    10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
                                                                                                                                                                                 188 EPHG------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGP_SHEEP STANDARD; PRT; 539 AA.

Q28542; Q28543;
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Estrus-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                  69;
                                                                                                    (POTENTIAL)
                                                                                                                                DB 1; Length 537;
                                                                                        OVIDUCT-SPECIFIC GLYCOPROTEIN.
                                                                                                                               22.1%; Score 685.5; DB 1; Length 5 33.3%; Pred. No. 1.3e-30; ive 95; Mismatches 183; Indels
                                                                                                    199 N-LINKED (GLCNAC. . .) (PC
59617 MW; CFDCEE6F0212D791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 TPTPT-TP-----TPAPTTSTPSP-----TTTEHTSETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 IATPIRIPLSFGRHTAAPEGKTESPGEKPLTIVGHLAVSP
PIR; S57197; S57197.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001259; Glyco_hydro_184.
Pfonon; PR00704; Glyco_hydro_18; 1.
SWART; SW00636; Glyco_hgro_18; 1.
SWART; SW00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Signal.
SIGNAL
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SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oviducal glycoprotein) (OEGP).
                                                                                                                                                    Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caprinae; Ovis.
                                                                                  18
537
399
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19 5
399 3
537 AA;
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Marshall J.T.A., Nancarcow C.D., Brownlee A.G.;

Marshall J.T.A., Nancarcow C.D., Brownlee A.G.;

"Cloning and sequencing of a CDNA encoding an ovine
costrus—associated oviducal protein.";

"Exprod. Fertil. Dev. 8:305-310(1996).

"I FUNCTION: Binds to cocyte zona pellucida in vivo. May play a role
in the fertilization process and/or early embryonic development.

"I SUBCELLULAR LOCATION: Secretory granules.

"I TISSUB SPECIFICITY: Oviduc.

"I TISSUB SPECIFICITY: Oviduc.

"I TISSUB SPECIFICITY: Oviduc.

"I DEVELOPMENTAL STAGE: Levels are highest in the fimbria and ampulla
te strins and nday 1 of pregnancy, when gamete transport and
fertilization occurs in the E2-dominated fallopian tube. Levels
decline significantly on day 2 and undergo a further significant
reduction on day 3 of pregnancy coincident with transport of the
embryo from the oviduct to the uterus, a reproductive stage
associated with rising progesterone levels.

"I SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Biolinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                    Desouza M.M., Murray M.K.;
"An estrogen-dependent secretory protein, which shares identity with chitinases, is expressed in a temporally and regionally specific manner in the sheep oviduct at the time of fertilization and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.0%; Score 685; DB 1; Length 539; 33.8%; Pred. No. 1.4e-30;
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122 K -> N (IN REF. 2).
282 A -> V (IN REF. 2).
375 A -> V (IN REF. 2).
520 I -> T (IN REF. 2).
59535 MW, F35000269987C193 CRC64;
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InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001279; Glyco hydro_18AS.
Péan; PP00704; Glyco hydro_18; 1.
ProDom; PD000471; Glyco hydro_18; 1.
SMMRT; SW00636; Glyco_18; 1.
SMART; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Signal.
                                                                                                                                                                                                                                                                                                              STRAIN=Merino, TISSUE=Oviduct;
MEDLINE=96329120; PubMed=8726871;
MEDLINE=95269691; PubMed=7750470;
                                                                                                                                                                                                        Endocrinology 136:2485-2496(1995)
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us-09-662-293-18.rsp

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Paquette Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                         Matches 141; Conservative
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CHAIN
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SEQUENCE
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STRAIN=FVB/N, TISSUE=Breast;
MEDLINE=95060797; PubMed=7970700;
Morrison B.W., Leder P.;
Morrison B.W., lette murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
Oncogene 9:3417-3426(1994).
                                                 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                           228 PLFSLPGDPK-----SSAYAMSYWRQLGVPPEKLLMGLPTYGRTFHLLRASQNELGAGA
                                                                                                                                                                                                           KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                      282 AGPASPGKYTKQAGFLAYYEVCSFVQRAKKRWINDQY--VPYAFKGKEWVGYDDAISFGY
                                                                                                                                                                                                                                                                                                                             340 KAFFIKREHFGGAMVWTLDLDDFRGNFCGTGPFPLAHTLNNLLVNDEFSS-----
                                                                                                                                                                                                                                                                                                                                                                                             TPTP----TTTPTTTPTTTPSPTTPSPTTPSPTTP-----TTTPSPTTPTTPSPT
                       EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLPDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                                                                   KLAFLKELGVSGVMVWSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
(GP-39) (BRD39 protein).
CHILL OR BRD39.
Buks mysota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells
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-!- SUBCELLULAR LOCATION: Extracellular (By similarity).
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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PIR, S61551; S61551.
MGD, MGI:1340899; Chi311.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18.
Probon; PD000471; Glyco_hydro_18; 1...
SMART; SM00636; Glyco_18; 1...
PROSTIE; PS01055; GITINASE_18; FALSE_NEG.
Glycoprotein; Signal.
1 21. POTENTIAL.
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Q61362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 FLKGAEVHRLSNE--KVPFATKGNQWVGYEHKESVKNKVGFLKEKKLAGAMVWALDLDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 YKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF----EP--HGYLLTAAVSPGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH
                                                                                                                                                                                                                                                             34 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDBYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                           Gaps
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (2P-0)
                                                                                                                                                                                           34;
                                    (POTENTIAL)
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                                                                                                                         21.9%; Score 680; DB 1; Length 381; 37.1%; Pred. No. 1.8e-30; ive 75; Mismatches 130; Indels
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Suzuki K., Sendai Y., Onuma T., Hoshi H., Hiroi M., Araki
"Molecular characterization of a hamster oviduct-specific
381 CHITINASE-3 LIKE PROTEIN 1.
60 N-LINKED (GLCNAC. . .) (POT
43001 MW; EF6581E8184F0450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671 AA
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413

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    340 KAMFVKKEHFGGAMVWTLDMDVRGTFCGNGPFPLVHILNELLVRAEFNSTPLPQFWFTL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------PTTTP----SPTTPTPTPAPTTSTPSPTTTEHTSETP 494
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                                                                                                                                                                                                                                                                                                                                                                                                                         14 GPSTTTPTTPTTTPTTTPTTPTTPSPTTP--------TTTPSP---TTPTTTPS
                                                                                                 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                            PLYKRPDETDELHTYFNVNYTMHYYLMNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
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                DMAANPTYROOFIOSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and characterization of a mouse oviduct-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein).
OVGP1 OR OGP OR CHITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ICR; IISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendai Y., Komiya H., Suzuki K., Onuma T., Kikuchi M., Hoshi H.,
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InterPro; IPR001579; Glyco hydro 18AS.
Pfam; PF00704; Glyco hydro 18; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD000471; Glyco_hydro_18; 1.
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01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
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MGD; MGI:106661; Ovgp1.
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SEQUENCE FROM N.A.
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Q62010;
                    128
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                             zona pellucida-binding glycoprotein.";
Biochem. J. 295:437-445(1993).
-!- FUNCTION: Binds to occyte zona pellucida in vivo. May play a role in the fertilization process and/or early embryonic development.
Might act as a protective secretion influencing the first steps of the reproductive process necessary for the normal triggering of fertilization and early embryonic development.
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Malette B., Bleau G.;
"Biochemical characterization of hamster oviductin as a sulphated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: Oviduct.
-!- PTM: HIGHLY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED.
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 671;
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H -> I (IN REF. 4).
D -> G (IN REF. 2 AND 3).
R -> Q (IN REF. 2 AND 3).
F -> Y (IN REF. 2 AND 3).
Q -> L (IN REF. 2 AND 3).
MISSING (IN REF. 2 AND 3).
T -> I (IN REF. 2 AND 3).
W; BBSTEOES14EC1972 CRC64;
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33.3%; Pred. No. 3.4e-30;
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InterPro; IPR01123; Glyco hydro 18.
InterPro; IPR01123; Glyco hydro 18.
Pram; PR00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SMART; SM0036; Glyco hydro 18; 1.
SMART; SM0036; Glyco 18; 1.
SPROSITES; CS01095; CHTMINASE 18; FALSE NEG.
Glycoprotein; Fertilization; Repeat; Signal.
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671 AA;
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characterization of an estrogen-dependent human oviductal

SEQUENCE FROM N.A., AND VARIANT glycoprotein."; Biol. Reprod. 51:685-694(1994)

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                                                                                                                                                                                                                                                                                                                                                                                               264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 VQRAKKH--WIDYQYVPYAFKGKEWLGYDDIISFSYKAMYVKREHFGGAMYWTLDMDDVR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 TEVLITIDIIKILPPGGEAMTTEVHRRYENMTTVPSDGSVTPGGTASPRKHAVTPENNTMA 473
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                                                                                                                                                                                                                                                    34 RIVCYVGTWSVYHKVDPYTI -- EDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNS 91
                                                                                                                                                                                                                                                                        23 KLVCYFTNWA-HSRPGPASIMPHDLDPFLCTHLIFAFASMSNNQI---VAKNLQDENVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 WRKLGTPADKLIMGFPTYGRNFYLLKESKNGLQTASNGPASPGKYTKQAGFLAYYEVCSF
                                                                                                                                                                                                                                                                                                                                                                                                                                          205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
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                                                           OVIDUCT-SPECIFIC GLYCOPROTEIN.

21 X 7 AA TANDEM REPEATS OF S-K-T-T-
[TAP]-G-[IV].
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012889; 015841; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 0viduct-specific glycoprotein precursor (Oviductal glycoprotein) (Oviductin) (Estrogen-dependent oviduct protein) (Mucin 9).
                                                                                                                                                                                                                       82;
                                                                                                                                                                                         DB 1; Length 721;
                                                                                                                                                                                      21.9%; Score 680; DB 1; Length 72
33.7%; Pred. No. 3.6e-30;
ive 79; Mismatches 184; Indels
                                                                                                                                                37246C8F01665652 CRC64;
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SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHTINASE 18; FALSE NEG.
Glycoprotein; Fertilization; Repeat; Signal.
SIGNAL
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469
721 AA;
                                                                                                                                                                                                       Best Local Similarity
Matches 175; Conserv
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486
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CARBOHYD
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MEDLINE=95119256; PubMed=7819450; Arias E.B., Verhage H.G., Jaffe R.C.; "Complementary deoxyribonucleic acid cloning and molecular

SEQUENCE FROM N.A. TISSUE=Oviduct;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 IMACIGLANASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                      Coville G.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Binds to occyte zona pellucida in vivo. May play a roll in the fertilization process and/or early embryonic development.
-- SUBCELLULAR LOCATION: Secretory granules.
-- TISSUE SPECIFICITY: Oviduct.
-- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 668; DB 1; Length 678; 33.1%; Pred. No. 1.5e-29; Live 91; Mismatches 192; Indels
                                                                   Jaffe R.C.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew, HGNC:8524, OVGP1.

MIM; 603578;

GO:0007565;

InterPro; IPR001223; Glyco_hydro_18,

InterPro; IPR001579; Glyco_hydro_18,

InterPro; IPR001579; Glyco_hydro_18,

Probom; PD000471; Glyco_hydro_18; 1.

SWART; SM00636; Glyco_18; 1.

PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                  EMBL; U09550; AAA86946.1; -... EMBL; U58010; AAB04126.1; -... EMBL; U58001; AAB04126.1; -... EMBL; U58002; AAB04126.1; JOINED. EMBL; U58003; AAB04126.1; JOINED. EMBL; U58006; AAB04126.1; JOINED. EMBL; U58006; AAB04126.1; JOINED. EMBL; U58006; AAB04126.1; JOINED. EMBL; U58006; AAB04126.1; JOINED. EMBL; U58008; AAB04126.1; JOINED. EMBL; U58008; AAB04126.1; JOINED. EMBL; U58008; AAB04126.1; JOINED.
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                                                                                                            SEQUENCE FROM N.A.
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mononuclear cells, or fibroblasts.

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                           109 TWLSTFANREKFIASVISLLRTHDFDGLDLFFLYPGLR-GSPMHDRWTFLFLIEBLLFAF
                                                                                                                                                                                                                          ||-----SSAYANNYWRKLGAPSEKLIMGIPTYGRTFRLLKASKNGLQARA
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MEDLINE=94064658; PubMed=8245017;
Hakala B.E., White C., Recklies A.D.;
Human cartilage gp.39, a major secretory product of articular chondrocytes and synovial cells, is a mammalian member of a chitinase protein family.";
Biol. Chem. 268:25803-25810(1993).
                                                                                               188 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLPDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                                            PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
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DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF
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Nyirkos P., Golds E.E.;
"Human synovial cells secrete a 39 kDa protein similar to a bovine
"Human synovial cells secrete a 39 kDa protein similar to a bovine
mammary protein expressed during the non-lactating period.";
Biochem. J. 269:265-268(1990).
-!- FUNCTION: May play an important role in the capacity of cells to
-sespond to and cope with changes in their environment.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Extracellular.
-!- TISSUE SPECIFICITY: Present in articular chondrocytes, synovial
cells as well as in liver. Undetectable in muscle tissues, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C3L1_HUMAN STANDARD; PRT; 383 AA.
913622; P30923;
01-JUL-1993 (Rel. 26, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 QTGFVVLVLLQCC------SAYKLVCYYTSWSQYREGDGSCFPDALDRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIED-IDPFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDDLASISCKLAFLKELGVSGVMVWSLENDDFKG-HCGP--KNPLLNKVHNMI
pancreas, mononuclear cells, or fibroblasts.
-!- PTM: Glycosylated.
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHITINASE-3 LIKE PROTEIN 1.
N-LINKED (GLCNAC. . .) (POT
76ADD8298EEEC2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005012; F:extracellular matrix structural con interPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; P0000471; Glyco_hydro_18; 1.
SWART; SW00636; Glyco_18; 1.
SWART; CHITINASE_18; FALSE_NEG.
Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%; Score 662; DB 1; 34.9%; Pred. No. 1.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; M80927; AAA16074.1; -...
EMBL; Y08374; CAA69661.1; -...
EMBL; Y08375; CAA69661.1; JOINED.
EMBL; Y08376; CAA69661.1; JOINED.
EMBL; Y08377; CAA69661.1; JOINED.
EMBL; Y08378; CAA69661.1; JOINED.
EMBL; Y08378; CAA69661.1; JOINED.
FIR; A49562; A49562.
Genew; HGNC:1932; CHI311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 AA; 42613 MW;
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Best Local Similarity 34.9°
Matches 144; Conservative
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Ź 623

PRT;

STANDARD;

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228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a recombinant complementary DNA to a baboon (Papio anubis) estradiol-dependent oviduct-specific glycoprotein.";
Mol. Endocrinol. 5:356-364(1991).
-!- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Mismatches 200; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Oviduct;
MRDilNE=98244335; PubMed=9584944;
WRDilNE=98244335; PubMed=9584944;
Verhage H.G., Fazleabas A.T., Mavrogianis P.A., O'Day-Bowman M.B.,
Donnelly K.M., Arias B.B., Jaffe R.C.;
"The baboon oviduct: characteristics of an oestradiol-dependent
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
           01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Bstrogen-dependent oviduct protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 OVIDUCT-SPECIFIC GLYCOPROTEIN.
402 N-LINKED (GLCNAC. . .) (POTENTIAL)
441 N-LINKED (GLCNAC. . .) (POTENTIAL)
69291 MW, 9E21CE481FFF1268 CRC64;
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Oviduct;
MEDINE=91367180; PubMed=1716345;
Donnelly K.M., Fazleabas A.T., Verhage H.G., Mavzogianis P.A.,
Jaffe R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 654.5; DB 1; Length 623; 30.7%; Pred. No. 7.6e-29;
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InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001229; Glyco_hydro_18AS.

Pfm; PF00704; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

ProDom; P000536; Glyco_hydro_18; 1.

PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Signal.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 oviduct-specific glycoprotein.";
Hum. Reprod. Update 3:541-552(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59903; AAB39765.1; -.
                                                                                          OVGP1 OR OGP.
Papio anubis (Olive baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                      Cercopithecinae; Papio.
NCBI_TaxID=9555;
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Matches 181;
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409
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188 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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                                                                                                                                     168 RKEALLTWRPRLLLSAAVSGVPHIVQTSYDVRFLGRLLDFINVLSYDLHGSWEKFTGHNS
                                                                                                                                                                                                                                                             ||: |:: | SAYAMNYWRKLGAPSEKLIMGIPTYGRIFRLLKASKNGLQATA
                                                                                                                                                                                                                                                                                                                                                   301 KGMSPPGFISGEEGVLSYIELCQLF--QKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASI
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Search completed: March 22, 2004, 06:53:05 Job time : 22.2868 secs

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Q9u6r7 dermatophag
044079 anopheles g
Q8ish5 araneus ven
017412 aedes aegyp
Q9w2z3 drosophila
Q9qqq4 bombyx mori
Q8wp05 tenebrio mo
Q8wr52 bombyx mori
015993 penaeus jap
Q9gr93 bombyx mori
Q9gr05 bombyx mori
                                                                                                  March 22, 2004, 06:39:53; Search time 111.679 Seconds (without alignments) 1568.003 Million cell updates/sec
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                                                                                                                                                                        US-09-662-293-18
3107
1 MKTIYAILSIMACIGLMNAS......IMPCPPGTIWQQEKLFCIGE 555
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                  1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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No.
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	; 555 AA.	PRT;	NARY;	PRELIMINARY;	17 27 2906R7 2906R7	RESULT 1 Q9UGR7 ID Q9U AC Q9U	ROHKI
	ALIGNMENTS	ΑI					
Q8bkl8 mus musculu	F8	1 Q8BKL8	389 1	N	687	45	
4 mus	184	¥ ⁻			687		
Q9vzv2 drosophila O9w2m6 drosophila	[7] <u>v</u>	O9W2W6		90	702.5	4 4 2 4	
Q8my79 haemaphysal	<u>م</u>	_		9.		41	
	90			8.8	708.5	40	
Q8w8ys grossina mo Q9w092 drosophila	0.2	OSWO92	484 504 504	22.0	710	3 6 3 6	
3 penaeus	<u>ب</u>			3.1	717	37	
	.01			3.3	722.5	36	
O8ms85 drosophila	. LO				723.5	3.0	
Q9h3v8 homo sapien	∞ r	Q9H3V8		9.10	732.5	93	
	787	m		3.6	733	32	
Q9d803 mus musculu	103	11 0908		3.6	734.5	31	
O99ph2 mus musculu	H2	11 099PH2		7.7	736.5	ט ה ס	
Ol3231 homo sapien	=	•		3.8	738	28	•
Q7zv48 brachydanio	748			4.3	754	27	
Q861z2 lutzomyia l		5 Q86LZ2		: 5.	762.5	5 2 2 2 3	
횩.		P91731		٠. د.	787	2.2	
Q9y0d4 penaeus mon	4.			5.4	790	23	
penaeus	2			5.7	798	22	
chelo		5 02373		. 6.	805	21	
O17411 apples approx			_			000	
Ogy44 spodoptera	4.4	09GV44		0.03	814.5	1 1	
Q8mtk0 choristoneu	8	Q8MTK0	557 5	6.5	823.5	17	

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								Acari,	lgoidea	,											bonds;													555;	0;
					(a)			hnida; 1	ia; Ana						n from		abases.				glycosyl bonds;	1											CRC64;	Length	Indels
	AA.			update)	annotation update)	ı		Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;	Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea	1				.; :	98 kDa Allergen		(AUG-1999) to the EMBL/GenBank/DDBJ databases				uo 6	IEA.												DB 5;	Freq. No. 2.9e-186; Mismatches 0;
	555 A		~	quence	notatic		t mite)	licerat	ata; Pe					McCall	98 kDa		nBank/D		₫.	EA.	y, acti	bolism;	, IEA.	rA.		AS.							0E4564A1A459B30B	Score 3107;	ea. No. 2. Mismatches
	PRT;		Created)	Last sequence update)	Last am		Dermatophagoides farinae (House-dust mite).	da; che	Astigm	des.				Stedman K., McCall	n of a		EMBL/Ger		C:extracellular; IEA.	F:chitin binding; IEA.	F:hydrolase activity,	P:carbohydrate metabolism;	P:chitin metabolism; IEA.	bind PerA	ydro_18	InterPro; IPR001579; Glyco_hydro_18AS	8; 1.	0_18; 1			18; 1.				
	; χ.;		. 13,	13,	25,		nae (Ho	thropo	ormes;	phagoi	,			Stedm	rizatio	iae.";	o the	572.1;	racellu	in bin	colase	ohydra	in met	hitin	lyco h	lyco_h	lydro_1	o_hydr	.;	18; 1.	INASE		63238 MW;	100.08;	 60.
	PRELIMINARY;		(TremBLrel	TrEMBLrel.	(TrEMBLrel.	rgen.	ss farir	zoa; Ar	arcoptif	Pyroglyphidae; Dermatophagoides	••		4.A.	ter S.,	"Cloning and Characterization of a	Dermatophagoides farinae.";	-1999) t	EMBL; AF178772; AAD52672.1;	C:extr				P:chit)2557; C	31223; G	11579; G	Glyco_r	71; Glyc	; ChtBD2; 1	. Glyco	PROSITE; PS01095; CHITINASE]a	555 AA; 63		ğ
	PRI		_	_	03 (T)	alle	agoide	Meta	es; S	idae;	D=6954		FROM P	Hun (:	and Ch	agoide	(AUG	78772	05576	GO:0008061;	16798	05975	06030	IPR0	IPR0	IPR0	0704;	D0004	00494	00636	PS0109	se; H	255	; ;	imita:
-	Ó9UGR7	Q9UGR7;	01-MAY-2000	01-MAY-2000	01-OCT-2003	98kDa HDM allergen.	rmatoph	karyota	ariform	roglyph.	NCBI_TaxID=6954;	_	SEQUENCE FROM N.A.	Weber E.R., Hunter	loning	rmatoph	Submitted	; AF1	; GO:0005576;	. 60:00		90:00	; GO:0006030;	terPro;	terPro;	terPro;	am; PF0	ODOM; P.	SMART; SM00494;	ART; SM	OSITE;	ycosida	SEQUENCE	Query Match	best Local Similarity Matches 555; Conserv
RESULT		_	_						Ċ		•					_	-	•	-															Query	Matches
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drosophíla drosophíla penaeus van bombyx mand

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Chitinase.
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                                                                                                                                                         SEQUENCE
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                                                MKTIYALISIMACIGIMNASIKRDHNDYSKNPWRIVCYVGTWSVYHKVDPYTIEDIDPFK
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                                                                                                                                                       CTHLMYGRAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                                                                                     EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                                                                                                                               EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
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                       MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae (African malaria mosquito).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
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MEDLINE=98030563; PubMed=9360958;
Shen Z., Jacobs-Lorena M.;
"Characterization of a novel gut-specific chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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J. Biol. Chem. 272.2889-28900 (1997).
Biol. Chem. 272.2889-28900 (1997).
Birl. AF008575; AB897764.1; -.
BIR. T44445; T44445.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:00059061; F:hditin binding; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005010; P:chitin metabolism; IEA.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002537; Chitin bind PerA.
InterPro; IPR001579; Glyco_hydro_18AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 VGRYTREPGVMGYNEFCEKLATBAMDLRWSEEQQVPYAVRNNQWVGYDDLRSVQLKVKYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 YSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FSAMAASGELRKRFISDCVAFCORHGFDGIDLDWEYPAORDGNPLIDRDNHAQLVEEMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 APTT----STVAPGTTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 ITTEHTSETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC-----EFVNGGWWVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LSIMACIGLMNASIKRD-HNDYSKNPWRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM
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Han J.H., Kim S.R., Sohn H.D., Jin B.R.;
"Molecular cloning of a cDNA encoding the chitinase from the spider,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
NCBI_TaxID=182803;
                                                                                                                                                                                                                                                                    29,
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                 32.5%; Score 1008.5; DB 5; Length
38.4%; Pred. No. 4e-55;
ive 93; Mismatches 187; Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY120879; AAN39100.1; -.
                                                                                                                                                                    525 AA; 57211 MW; 3234360EEFF36165 CRC64;
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Pfam; PF01607; CBM 14; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00494; ChrBD2; 1.
PROSITE; PS01095; GHYCO_18; 1.
Glycosidase; Hydrolase.
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                                                                                                                                                                                                                      Query Match 32.5%;
Best Local Similarity 38.4%;
Matches 211; Conservative
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1057 PTRPPTS-----TTPETTRRPSTTTSTRRTTMTTT--TTTRRPTTRRTSAR 1104
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GO; GO:0008576; C:extracellular; IEA.

RG GO:0008061; F:chitin binding; IEA.

GO; GO:0008061; F:chitin binding; IEA.

GO; GO:0008061; F:chitin binding; IEA.

GO; GO:0008975; P:chitin binding; EA.

RG; GO:0006035; P:chitin actabolism; IEA.

RG; GO:0006035; P:chitin binding Pera.

RICEPPO; IPRO01223; Glyco_hydro_la.

RICEPPO; IPRO01223; Glyco_hydro_la.

RICEPPO; IPRO01579; Glyco_hydro_la.

REAM: FRO0104; Glyco_hydro_la.

RART; SM00494; ChtBD2; 3.

RART; SM00495; CHITINASE_la.

RART; SM00495; CHITINASE_la.

RART; SM00495; CHITINASE_la.

RARD; CARBOHYD 322 322 N-LINKED (GLCNAC. . ) (POTENTIAL).

RARD; CARBOHYD 322 322 N-LINKED (GLCNAC. . ) (ROTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                              | N-LINKED (GLCNAC. . .) (POTENTIAL) | 322 | 322 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 463 | 463 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 479 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 890 | 890 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 1338 | 1338 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 1479 | 1479 | N-LINKED (GLCNAC. . .) (POTENTIAL) | 1635 AA; 185993 MW; EALLGFB3AAC129FA (RC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.0%; Score 869; DB 5; Length 1635; 34.3%; Pred. No. 8.3e-46; ive 95; Mismatches 196; Indels 84
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - PESDKILMVDYAINYWIKNGTPKNKVILGMGTYGRSFTLANAANNGLGAATTGPGSAGP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAANPIYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 PHGLILSAAVSAGKOYIDIAYDIPGVAKYLDFINVMAYDLHGSWEKTAGHNAPLYERPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKEL
                                                                                                                                                                                                                                                                                                                             ||:|: |: |: || || || || || || || ACLLILLVAVAVSAQSRDRNQKKYKVVCYLGSWANYRGGEGKFLIEHIDPFLCTHVIYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWBNFYGHNAPLYKRPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPT
                                                                                                                                                                                                                                                                                                       12 ACIGLM--NASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila.";
Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes. NCBI TaxID=7159; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINES 99324849; PubMed=9662472; de la Vega H., Spectt C.A., Liu Y., Robbins P.W.; Chitinases are a multi-gene family in Aedes, Anopheles and
                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                Query Match 30.3%; Score 942; DB 5; Length 431; Best Local Similarity 43.6%; Pred. No. 4.6e-51; Matches 185; Conservative 78; Mismatches 135; Indels
                                                                                                                                                                           929439397B9BC923 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-CCT-2003 (TEMBLrel. 25, Last annotation update)
Probable chitinase 2 (EC 3.2.1.14).
  GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR00123; GIyco.hydro.la8.
InterPro; IPR001579; GIyco.hydro.la8s.
Pfam; PF00704; GIyco.hydro.la8; 1.
ProDom; PD000471; Giyco.hydro.ls; 1.
SWART; SW00636; GIyco.ls; 1.
PROSTIT: SR001055; GITTINASE 18; 1.
SEQUENCE 431 AA; 47238 MW; 929439397B9BC923 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aedes aegypti (Yellowfever mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF026492; AAB81850.1;
PIR; T14075; T14075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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RAMENINE-20180066; Bubbed=1073132;

RAMENINE-20180066; Buther S.E., Li P.W., Hoskins R.A., Galle R.F.,

RAMAGARIES P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RAMAGARIES P.G., Scherer B.G., Holt R.A., Galle W. Henderson S.N.,

RAMAGARIES P.G., Rogers Y.-H.C., Blazej R.G., Champe M., Feleffer B.D.,

RAMENCH, Doyle C. Baxter E.G., Helt G., Champe M., Feleffer B.D.,

RAMENCH, Doyle C., Baxter E.G., Helt G., Champe M., Feleffer B.D.,

RAMENCH D. Botchan M.R., Bouck J., Roketein P., Bolshakov S.,

Burtis N.C., Busam D.A., Danlae J., Bayraktaroglu L., Besaley E.M.,

Burtis N.C., Busam D.A., Danlae C., Davenport L.B., Davies P.,

RAMENCA D., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAMENCA D., Cawley S., Dahlke C., Perraz C., Ferriar C., Perriar C.,

RAMENCA D., Barden M., Davies M., Digan-Rocha S., Dunkov B.C.,

RAMENCA D., Beangalista C.C., Ferraz C., Ferriar S., Pletschmann W.,

RAMICH M., Raush F., Karpen G.H., Wei M.-H., Libeyam C.,

RAMEN D., Houston K.A., Helman T.J., Herriandez J.R., Harris M.L.,

RAMEN D., Houston K.A., Helman T.J., Herriandez J.R., Hockin M.,

RAMEN D., Houston K.A., Helman T.J., Herriandez J.R.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RAMEN M., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,

RAMEN M., Malshina N.Y., Milshina N.Y., Belled M.P., Moshrefi A.,

Ramazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rechel M. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,

Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,

Wang Z.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J.,

Williams S.M., Woodsey T., Walley K., Zhan G., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on glycosyl bonds; IEA.
                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4498 AA; 493096 MW; AEE65CE0AAB25489 CRC64;
                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005576; C:extracellular; IEA.
GO:0008061; F:chtin binding; IEA.
GO:0016798; F:hydrolase activity, acting on
GO:0005975; P:carbohydrate metabolism; IEA.
GO:0006030; P:chitin metabolism; IEA.
 PRT; 4498 AA
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InterPro; IPR001529; Glyco_hydro_18AS.
Pfam; PF001607; CBM_14; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SWART; SM00494; ChtBD2; 1.
SWART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
                                      Created)
                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                    (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 25, I
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 PRELIMINARY;
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                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                STRAIN=Berkeley;
                                                                                           CG2989 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase;
SEQUENCE 44
                   Q9W2Z3;
01-MAY-2000
                                                     01-MAY-2000
01-OCT-2003
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C STRAIN-Shunrei x Showgetsu;

X MEDLINE-20545518; PubMed=10984482;

MEDLINE-20545518; PubMed=10984482;

MIKHtani K., Sugasaki T., Shimada T., Kobayashi M., Gustafsson J.A.;

MIKHtani K., Sugasaki T., Shimada T., Kobayashi M., Gustafsson J.A.;

T "The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
I'm The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
I'm The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
I'm The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
I'm The Chitinase a Contain Bombyx mori, Contains a Novel Tc-
I'm The Chitin binding; IEA.

R G) G0:0008576; Ciextracellular; IEA.

R G) G0:0006576; P:chitin binding; IEA.

R G) G0:0006976; P:chitin meteabolism; IEA.

R G) G0:0006309; P:chitin meteabolism; IEA.

R InterPro; IPR002557; Chitin_bind_PerA.
                                                                                                                                                                                                                                                                                                                    342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 ----KEAMVEALGINEVAKPSGPQKPSRSRSRDNASNRNRLNGKTEAPLSSRRPSATR 478
                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 FHSSHEPSVNHHAPLYSL--BEDSEYNYDABLNIDYSIKYYLKAGADRDKLVLGIPTYGR 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GSDFKCEEEGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AYRRNQWVGYDDBAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIBAA----
                                                                                                                                                                                                                                                                                                                                                                                                                446 SPITPTITPSPITTT--------PSPITPTPTPTPAPITSTPSPTTEH
                                                                                              2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID
                                                                                                                                             33 QTLFLLCALAYCI------NEASSEG-RVVCYYTNWSVYRPGTAKFNP---QNIN
                                                                                                                                                                                                                                                                                           115 SLGGWYEGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCOLFOKE-EWH-IQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 NGDEKNSFECILGPSTTTPTTTTPTTTTT------TPSPTT---PTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPPTTPDP---------
                                                                                                                                                                                            58 PPKCTHLMY --- GFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELITMI
                                                                                                                                                                                                                                                                                                                                                                                         175 NYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 YHGGWENFYGHNAPLYKRPDETDELHTY ---FNVNYTMHYYLNNGATRDKLVMGVPFYGR
27.5%; Score 854.5; DB 5; Length 4498;
33.8%; Pred. No. 2.2e-44;
ive 88; Mismatches 188; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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  Query Match
Best Local Similarity 33.8
Matches 202; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitinase.
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09GQC4;
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2147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 NDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPT--PTTTPT-TPTTPT- 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2328 KPTPKPSTPPYEPQKPSTQKPSYGTTESPEPVMPPDSVPCRGRLFVADEKNCNQYYLCNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYL------VCEFVNGGWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLOEYKEDGLDLDWEYP----GSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDMAANPTYRQQFIQSVLD
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
insect Chitinase with multiple catalytic domains
                                                                                                                                                                                                                                                                                                                                                                                               Length 2838;
                                                                                                                                                                                                                                                                                                                                                                                               27.1%; Score 842; DB 5; Length 28 32.2%; Pred. No. 7.8e-44; ive 92; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                   SIGNAL 1 20 POTENTIAL.
CHAIN 21 2838 CHITINASE.
SEQUENCE 2838 AA; 321407 MW; 608B3F2A8E98B9B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----STITESTITE-SPIT-----PITESTITETITESTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V---HIMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 32.2%
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534
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                                                                                                                                                                                                                                                                                                 119 WYEGSEKYSDWAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394
                                                                                                                                                                                                                                                                                 59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG 118
                                                                                                                                                                                                                       1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP 58
                                                                                                                                                                                                                                         178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYKGTQWVGYEDPRSVEIKAMWIKEKGYLGAMTWAIDMDDFKGLCGEENPLIKLLH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|||||| : : ||| : : | || : : ADVHSPLYKRPHD-QWAYEKLAVNDGLNLWEKKGCPTNKLVVGIPFYGKSFTLSAGNNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDEKNSFECILGPSTT----TPTPTTTPTTTPTTPSPTTPSTTPSPTTPSTTTPSPTTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RITARPI--ITITKVPHGITEEDFDINVRPEVEEPPIENEVDNADV-CNSEDDYVPDKKE
                                                                                                                                                                                                                                                                                                                                                          GLGTYINKEAGGGDPAPYTNATGF -----WAYYEICTEVDADGSGWTKKWDEFGKCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----
                                                                                                                                                                                             Gaps
                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tenebrio molitor (Yellow mealworm).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Tenebrionidae, Tenebrio.
                                                                                                                                                              Query Match
27.3%; Score 847; DB 5; Length 544;
Best Local Similarity 36.5%; Pred. No. 5.2e-45;
Matches 207; Conservative 78; Mismatches 218; Indels
     InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pf01670; GRM_14; 1.
ProDom; PF001670; Glyco_hydro_18; 1.
ProDom; PF000471; Glyco_hydro_18; 1.
SMART; SM00444; ChtBD2; 1.
SMART; SM00485; Glyco_18; 1.
SMART; PF01095; CHTHINASE_18; 1.
Glycosidase; Hydrolase.
SEQUENCE 544 AA; 61069 MW; 89872DFC1DA23753 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 IHKYLVCEFVNGGWWVHIMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSKYWRC--VNGEGVQ--FSCQPGTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-00T-2002 (TrEMBLrel. 22, Created 01-0CT-2002 (TrEMBLrel. 22, Last 801-0CT-2003 (TrEMBLrel. 25, Last and Chiilnase precursor (EC 3.2.1.14).
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SEQUENCE FROM N.A.
Royer V., Fraichard S., Bouhin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343
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       343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDI
                                                 339 AYKGTQWYGYEDPRSVEIXMNWIXEKGYLGAMTWAIDMDDFKGLCGEENPLIKLLHKHMS
                                                                                                                                                                                                                                                                                                      459 PTTTPSPTTPTPTPTPTPAPTTSTPSPTTTE-----HTSETPKYTTYVDGHLIKCYKE
                                                                                                                                                                                                                                                                                                                                                                       445 TRITIARPIT-----TITIKVPHGITEEDFDINVRPEVEELPT-ENEVDNADV-CNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD--DNHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 FDGLDMDWEXPTQRGGSPD-DYDNFAILMAELKQALQPEGMLLTAAVSAGKATIDPAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 KELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRP-DETDELHTYFNVNYTMHYYLNNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 GDEKNSPECILGPSTITPTTTTTTTTTTTTPSPTTPTT----TPSPTTPTTTPSPTT
                                                                                                                                                                                                                         ------TYTVPPARTGHTTPTPEWARP-PSTPSDPSEGDPIPTTTTTVKPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pjchi-3.
Penaeus japonicus (Kuruma prawm).
Penaeus japonicus (Kuruma prawm).
Penaeus japonicus (Kuruma prawm).
Bukaryota Matazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Bucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Marsupenaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 GD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.0%; Score 837.5; DB 5;
34.8%; Pred. No. 1.7e-44;
ive 85; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 DDYVPDKKECSKYWRC--VNGEGVO--FSCOPGTIF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0015787; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001257; Chitin bind Pera.
InterPro; IPR001279; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
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01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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015993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 DLCTHLIYSFIGVTEKSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDVKFWVAVGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 WYEGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombyx mori (Silk moth).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 ADVHSPLYKRPHD-QWAYEKLAVNDGLALWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 GLGTYINKEAGGGDPAPYTNATGF-----WAYYEICTEVDADGSGWTKKWDEFGKCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Kinshu x Showa, TISSUB=Integument;
Abdel-Banat B.M.A., Koga D.;
"Alternative mRNA splicing generates heterogeneity within Bombyx mori
gene for chitinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on glycosyl bonds; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0008576; C:extracellular; IEA.

GO; GO:0008643; F:chitin binding; IEA.

GO; GO:0008643; F:endochitinase activity, acting on glycosyl bo GO; GO:000579; P:rhydrolase activity, acting on glycosyl bo GO; GO:000579; P:carbohydrate metabolism; IEA.

R GO; GO:000579; P:carbohydrate metabolism; IEA.

R InterPro; IRR001223; Glyco_hydro_l8.

R InterPro; IRR001223; Glyco_hydro_l8AS.

R FEam; PF001607; CBM 14; 1.

R FEAM; PF001607; Glyco_hydro_l8; 1.

R FEAM; PF001607; Glyco_hydro_l8; 1.

R FEAM; PF001607; Glyco_hydro_l8; 1.

R FROSITE; PS01095; Glyco_hydro_l8; 1.

R SWART; SM00634; CHYDO.] 18; 1.

R PROSITE; PS01095; CHITINASE_18; 1.

R SMART; SM00636; Glyco_l9 Domewria.

R SMART; SM00636; Glyco_l9 Domewria.
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                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                            01-WAR-2002 (TrEMBLrel. 20, Create 01-WAR-2002 (TrEMBLrel. 20, Last s 01-OCT-2003 (TrEMBLrel. 25, Last a Chitinase precursor (EC 3.2.1.14).
2499 VLDGSTMTLKPHDSW 2513
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Matches 207; Conservative
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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ID Q9GV05
AC Q9GV05;
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                                                                                                                                                         387
                                                                                                                                                                                            TVVDDPAMHEPYAYYFPMNNIWCSYDHAASVVTKAEYAKSKGLAGTMVWSVETDDFRGLC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IHC 403
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EMBL; ABD622914 BAB2017.1, -

R GO; GO:000861; F:chitin binding; IEA.

R GO; GO:0008801; F:chitin metabolism; IEA.

R GO; GO:0006030; F:chitin metabolism; IEA.

R GO; GO:0006030; P:chitin metabolism; IEA.

R GO; GO:0006030; P:chitin metabolism; IEA.

DR InterPro; IPR001223; Glyco_hydro_18.

DR InterPro; IPR001579; Glyco_hydro_18.

DR Pfam; PF01607; CBM 14; 1.

DR Pfam; PF01607; CBM 14; 1.

DR Pfam; PF01607; CBM 14; 1.

DR RATT; SW00494; ChtED2; 1.

DR SWART; SW00636; Glyco_hydro_18; 1.

DR RAST; SW00636; Glyco_18; 1.

DR RAST; SW00636; Glyco_18; 1.

DR RAST; SW00636; Glyco_18; 1.

DR ROSTIE; PS01095; CHITINASE 18; 1.

DR ROSSTIE; PS01095; CHITINASE 18; 1.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bombyx mori (Silk moth).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                       GPKNPLLNKVANMINGDEKNSFECILGPSTTTPTTPTTTTTTTPTTPTTTPTTTPTTPSP
                                                                                                                                                                                                                                                                                                                  354 H-----NRKYHLI----KTMVEVFGGGSITEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIQYDEYYNAPYGY---NDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
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                             TRDKLVMGVPPYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCOLFOKEEW
                                                                                                                                                                                                                                                                                                                                                                                                          TIPITIPSPITFITPSPITFITPTPAPITSTPSPITTSTPSFITTEHTSETFKYTTYVDGHLIKC
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STRALN=Kinshu x Showa; TISSUE=Integument;
Abdel-Banat B.M., Koga D.;
"Molecular cloning of Bombyx mori chitinase cDNA: a unique insert obase pairs reduced the apparent molecular mass of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Chitinase precursor (EC 3.2.1.14).
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Best Local S
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PKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG 118
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Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
Bombycidae, Bombyx.
NCBI_TaxID=7091,
                                                                                                                                                                                      338 AYKGTQWVGYEDPRSVEIKMNMIKEKGYLGAMTWAIDMDDFKGLGGENPLIKLLHRHMS
                                           DICTHLIYSFIGVTEXSSEVLIIDPELD-----UDKSGFRNFTSLRSKHPDVKFMVAVGG
                                                                                                                                       WYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL
                                                                                                                                                                                                                                                                                     ALVRELKDAR--BPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
                                                                                                                                                                                                                                                                                                                          166 YFVQELKRAFIRAGRGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGF
                                                                                                                                                                                                                                                                                                                                                                                                                            236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 GLGTYINKEAGGGDPAPYTNATGP-----WAYYEICTEVDADGSGWTKKWDEFGKCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 GYNDKIWYGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------THIVPPARIGHTIPIEWARP-PSTPSDPSEGDPIPITUKPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on glycosyl bonds; IEA.
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SIGNIBLEALIBHU X Showa hybrid; TISSUE=Integument;

MEDLINE=Z1124800; Pubmed=11222960;

A Abdel-Banat B.M.A., Koga D.;

"A genomic clone for a chitinase gene from the silkworm, Bomb structural organization identifies functional motifs.";

Insect Blochem (Mol. Biol. 31:497-508(2001).

EMBL; AB04835; BAB13481.1;

Insect Blochem (Mol. Biol. 31:497-508(2001).

R GO; GO:0008643; F:candechitinase activity; IEA.

GO; GO:0008643; F:chitin binding; IEA.

GO; GO:0008943; F:candechitinase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

RO; GO:000630; P:chitin bind PerA.

R InterPro; IPR00123; Glyco_hydro_las.

InterPro; IPR0123; Glyco_hydro_las.

InterPro; GMI (Glyco_hydro_las.)

R Probom; PD00041; Glyco_hydro_las.

R Probom; PD00041; Glyco_hydro_las.

R Probom; PD00041; Glyco_hydro_las.

R Probom; PD00041; Glyco_hydro_las.

R PROMNT; SM00494; ChtBD2; 1.
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Last annotation update)
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 GLGTYINKEAGGGDFAPYINATGF-----WAYYELCTEVDADGSGWTKKWDEFGKCPY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 GYNDKIWYGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTTTPSPTTPTPTTTPTPAPTTSTPSPTTTB-----HTSETPKYTTYVDGHLIKCYKE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 TRİTARPİT.------TİTKVPHGITEEDFDINVRPEVEELPT-ENEVDNADV-CNSE 492
                                                                                                                                                                                                                                                                                                                                               118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 ADVHSPLYKRPHD-QWAYEKLNVNDGLNLWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 284
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chitinase-like protein.
Bombyx mori (Silk moth).
Bukaryxt mori (Silk moth).
Bukaryxta, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Nopptera, Endoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
                                                                                                                                                                                                                                                                                                                                             59 FKCTHLMYGFAKIDBYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG
                                                                                                                                                                                                                                                                                                                                                                          51 DLCTHLIYSFIGVTEKSSEVLIIDPELD-----VDKSGFRNPTSLRSKHPDVKFWVAVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RSKIKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY
                                                                                                                                                                                                                                                                                           MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP
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                                                                                                                                                                                                                  83;
                                                                                                                                                                 Query Match
Best Local Similarity 35.9%; Pred. No. 2.1e-44;
Matches 207; Conservative 78; Mismatches 208; Indels 83
                                                                                                                            DE29675D83AEC2EF CRC64;
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SMART; SW00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
Glycceidase; Hydrolase; Signal.
20
POTENTIAL.
                                                                                                          CHITINASE
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60982 MW;
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543 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 WABGGSKYSHWVAQKSTRMSFIRSVVDFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 ALVRELKDAF--BPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----
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R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0008061; F:chitin binding; IEA.

R GO; GO:0008061; F:chitin binding; IEA.

R GO; GO:0005975; P:carbolage activity, acting on glycosyl bonds; IEA.

R GO; GO:0005975; P:carbolage metabolism; IEA.

R GO; GO:0006030; P:chitin metabolism; IEA.

R InterPro; IPR001257; Chitin bind_PerA.

R InterPro; IPR001257; Chitin bind_PerA.

R InterPro; IPR001257; Chitin bind_PerA.

R Fine Pro; IPR001257; Glyco_hydro_18.

R Pfam; PF00704; Glyco_hydro_18; 1.

R ProDom; PD000471; Glyco_hydro_18; 1.

R SMART; SM006494; ChEBD2; 1.

R SMART; SM00636; Glyco_hydro_18; 1.
                                                      IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score 837.5; DB 5; Length 35.9%; Pred. No. 2.2e-44; ive 78; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        77D26D014875F3E2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
CG9307 protein (LP08894P).
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                                                                                                                                                                                                                                                                                                                                                                                                        565 AA; 63394 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 35.9
nes 207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Glycosidase; Hydrolase
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SUCURALE TOWN WAY.

READLINESTROY NAME

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RADDINESTROY NAME

RADDINESTROY SCHERE S. HOLF R.A., EVARS C.A., GOCCAYNE J.D.,

RADDINESTROY SCHERE S.E., RIGHARGS S., ASHDURDER M., HENGELSER S. RIGHARGS S., ASHDURDER M., HENGERS S.N.,

BUTCHON G.G., WORTHMAN J. R., YANGELI M.D., ZARNG Q., CHEN L.X.,

RADATION G.G., WORTHWAN J. HELF G., CHANDE M., PRESEIVER B.D.,

RADATION C., BARGER Y.H.C., BLACK S., CHENDER M., PRESEIVER B.D.,

RADATION R. BERNOR J., BEWIND S., RESEIVER S., RESIDENCH C., BARGHAND D.,

RADATION R. BORDER P.J., BANDINE G., DANGER P., BOSSIGN S.,

RADELIS K.C., BUSAM D.A., BURDER H., CAGIGUE B., CHERT A., CHANGE P.,

RADATION R., CAWAGE S., DANINE C., DAVERDOR J., DOLINES P.,

RADATION R., CAWAGE S., DANINE C., DAVERDOR J., DOLINES P.,

RADATION R., CAMAGE S., DANINE C., DAVERDOR J., DICKER A., CHANGE P.

RADATION R., DELICHER A., DENGE M., DOLINES P., HONGE S.,

RADATION R., GOME F. GORTELI J.H., GAZI W.S., GELBART W.M., GLASSER M.,

ROGGOR K., MORDER P., GARFEL J.H., GAZI K.S., HONGE S.,

RADATION R., ACHIER F., KARPEN T.J., HERNARDER J., RECKIM R. K.,

RADATION R., KALLER F., KARPEN T.J., HERNARDER J., ROCK M., RELANDER J., LEI Y., LEVITCKHY A., LIN T., LIANGE S., LIANGY Y., LIN X.,

RADATION R., MUSHAIN R., RADATION G., MOLEGOM M.P., MORDER S., MORDER S.,

RADATION G., WILSHIMA N.V., MONDARY C., MOLEGOM M.P., MORDER S., SHORE H.,

RADATION G., MILSHIMA N.V., MONDARY C., MOLEGOM R., WARDER G., SHORE R.,

RADATION R., MORDER S., WANGER S., WANG R., WANG R., WANGER S., SHORE R., WORLD S.K., MONGAGE T., WORLDSCH T., WALDER R., WANGER S., MANGERSCH D. R., STERNER R., RECHOR R., SHORE R., WANGERSCH D., STANGER S., SHORE R., WANGERSCH R., STANGER S., SHORE R., WANGERSCH R., STANGER R., RESERBER D., SHORE R., WANGERSCH R., STANGER S., STANGER S., WANGERSCH D., STANGER S., WANGERSCH D., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M., STANGER S., WANGERSCH M
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Berkeley;
A Stapleron M., Barkstein P., Hong L., Agbayani A., Carlson J.,
A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
The Nuco O., Pacleb O., Paragas V., Park S., Phouanenavong S., Wan K.,
A. Vu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BRBL; AR003701; AAF54987.1; -.
RPBL; AR003701; AAF54987.1; -.
RPBL; AV061553; AAL29101.1; -.
RPJBL; AR003701; Printin binding; IEA.
GO, GO:0005076; Printin binding; IEA.
GO, GO:0005075; Printin metabolism; IEA.
RO; GO:0006030; Printin metabolism; IEA.
RO; GO:0006030; Printin metabolism; IEA.
RICEPPO: PRR002557; Chitin bind Pera.
RICEPPO: IPR001223; Glyco_hydro_18.
RICEPPO: IPR001223; Glyco_hydro_18.
RICEPPO: IPR001223; Glyco_hydro_18AS.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
(VED_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 AA; 67050 MW; 8DC8469D3F732593 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD000471, Glyco hydro 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00494; ChtEB2; I. SMART; SM00494; ChtEB2; I. SMART; SM00636; Glyco_18; 1. GlycoSITE; PS01095; CHITINASE_18; 1. Glycosidase; Hydrolase; Hydrolase; Hydrolase; SEQUENCE 595 AA; 67050 MW; BDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01607; CBM 14; 1. Pfam; PF00704; Glyco hydro 18; 1.
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22;
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                                                                                                                                                                                                                                                                                                                                                                                            320 BLC-QLFQKEE-WHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWS 377
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                                                                                                                               88 NHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFL 147
                                                                                                                                                  203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTTP----SPTTPTT-----TPSPTTPTTPS--PTTPTTPSPTTPF-- 473
                                                                                                                                                                                                                                                                204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH 263
                                                                                                 81
                                                                                                                                                                                             148 QEYKFDGLDLDWEYPGS---RLGNPKIDKQNYLALVRELKDAF--EPHGYLLTAAVSPGKD
                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., II P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Strandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrill J.F., Agbayani A., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 TPAPTISTPSPITTEHTSETPKYTTY-------VDGHLIKCYKEGDIPHP
                                                               29 SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHIMYGFAKIDEYKYTIQVFDPYQDD
                                                                                  LENDDPKGHCGPKNPLLNKVH-NMINGDEKNSFECILGPSTTTPTFT----TTPTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Butoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
 27.0%; Score 837.5; DB 5; 35.2%; Pred. No. 2.3e-44; ive 84; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 TNIHKYLVCEFVNGGWWVHIMP----CPPGT 543
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
   Query Match
Best Local Similarity 35.24
Matches 201; Conservative
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CG9357.
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Q9W2M7
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dawi I., Dietz S.M.,

Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

A Dourbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

A Jolek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wernandez J.R., Houck J.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kanj D., Lai Z.,

A Markel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLedd M.D., Mosherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Shies B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shies B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstone E., Wang A.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhang G., Zhang G.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhang G.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhang G.,

RE Sheng X.H., Zhong F.N., Zhong W., Zhang G., Zhang G.,

RE Shence 287:2185-2195(2000)

BR HSSP POPSES: MARRIS A. W., Rober B. W., Rubin G. W., Venter J.C.;

RE SERL, REGEL 287:2185-2195(2000)
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26.8%; Score 832; DB 5; Length 460;
Best Local Similarity 33.7%; Pred. No. 3.7e-44;
Matches 183; Conservative 87; Mismatches 175; Indels
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--KCAYDRFTALKQQNANLKAILAVGGWNEGSPKYSKWAADPVLRNRFITSSIELLKKHG 116
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235 QQQLNVDAVVKYWLKAGAPAEKLILGVPFYGRSFTLATAEGNQPGAPHIGKGIAGNYSRE 294
                                                                                                    313 EGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSG 372
                                                                                                                                                                        295 PGVLGYNELCEMMEREEWTQKWEATQQVPYAYRQRGWVGYEDPRSLALKAQYVMDNHLGG 354
                                                                                                                                                                                                                                            373 VMVWSLENDDFKGHCGPK-NPLLNKVHNMINGDEKNSFECILGPSTTTPTTPTTPTT 431
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"Cloning and characterization of a cDNA encoding a chitinase from heperopancreas of the Penaeus vanameil (Crustacea, Decapoda).";

"Cloning and characterization of a cDNA encoding a chitinase from the peropancreas of the Penaeus vanameil (Crustacea, Decapoda).";

"Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

"EMBL, AF315689; AAN74647.1; ...

"GO, 60:0005576; Crextracellular; IEA.

"GO, 60:0005757; Printin binding, IEA.

"GO, 60:000577; Printin binding, IEA.

"GO, 60:000577; Printin metabolism; IEA.

"GO, 60:0006375; Printin metabolism; IEA.

"GO, 60:0006375; Printin metabolism; IEA.

"GO, 60:0006375; Printin metabolism; IEA.

"GO, 60:0006375; Printin metabolism; IEA.

"GO, 60:0006375; Printin metabolism; IEA.

"GO, 60:0006077; Glyco_hydro_18, 1.

"DR Promo, PROMO471; Glyco_hydro_18; 1.

"RART; SM00494; ChtBD2; 1.

"BR RART; SM00494; ChtBD2; 1.

"BR ROSITE; PS01095; CHTINASE 18; 1.
                                                                                                                                                                                                                                                                                   355 IMIWSLESDDFRGTCGQQPYPLLHBINRVLFGG------
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Litopenaeus.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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llarity 34.2%; Pred. No. 4.1e-44;
Conservative 87; Mismatches 174;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 22, 2004, 06:59:34 ; Search time 4.09116 Seconds (without alignments) 1265.926 Million cell updates/sec

US-09-662-293-13 105 1 DPAKGMSPPGFIVGEEGVLS 20 Title: Perfect score: Sequence:

Scoring table:

1049977 seqs, 258955339 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1049977 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli	Sequence 13, Appl	Sequence 41, Appl	Sequence 35, Appl	Sequence 38, Appl	Sequence 21, Appl	Sequence 15, Appl	Sequence 18, Appl	Sequence 238601,	Sequence 181344,	Sequence 483, App	Sequence 6, Appli	Seguence 6, Appli	Sequence 6, Appli	Sequence 2, Appli
DI	US-10-218-743-4	US-10-218-743-13	US-10-218-743-41	US-10-218-743-35	US-10-218-743-38	US-10-218-743-21	US-10-218-743-15	US-10-218-743-18	US-10-424-599-238601	US-10-424-599-181344	US-09-925-302-483	US-10-067-615-6	US-1:0-076-754-6	US-10-076-773-6	US-08-916-625B-2
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% Query Match Length DB	20	20	490	509	509	536	555	555	143	69	57	350	350	350	411
% Query Match	100.0	100.0	96.2	96.2	96.2	94.3	94.3	94.3	47.6	46.7	45.7	45.7	45.7	45.7	45.7
Score	105	105	101	101	101	66	<u>გ</u>	<u>გ</u>	20	49	48	48	48	48	48
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-09-828-73	-09-757-4	09-874-13	39-887-879-	11-	9-99	US-10-211-462-67	.0-039-785	0-005-8	0-067-615	0-052-798	.0-076-7	.0-076-7	.0-207-6	0-314-41	0-242-3	88-9	10-322-	10-13	10-292-	US-10-333-712-4	10-4	-09-757-4	US-09-811-088-4	US-10-314-	Þ	US-10-424-599-16974	US-10-424-599-26	US-10-425-114-5729	US-09-738-626-6409
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48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	46	46	45	45
16	17	18	19	20		22	23	24	25	26	27	28	29	30	31	32	33	34	35	.36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: MCCALI, Catherine A.
APPLICANT: MCALI,
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Exica R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1998-04-17
SPRIOR FILING DATE: 1998-04-17
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100.0%; Score 105; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-4
Sequence 4, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
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; TYPE: PRT;
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35
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; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 DPAKGMSPPGFITGEEGVLS 317
                                                                                                                                                                                                                                   279 DPAKGMSPPGFITGEEGVLS 298
                                                                                                                                                       1 DPAKGMSPPGFIVGEEGVLS 20
                         Best Local Similarity
Matches 19; Conserv
Query Match
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| SGUENCE 41, Application US/10218743
| Publication No. US2030096779A1
| GENERAL INFORMATION:
| APPLICANT: McCall, Catherine A. APPLICANT: McCall, Catherine A. APPLICANT: Weber, Eric R. TITLE OF INVENTION: NOVEL DERWATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: NOVEL DERWATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS FILE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
| CURRENT PPLICATION NUMBER: US/09/29, 225 |
| PRIOR APPLICATION NUMBER: 60/098, 909 |
| PRIOR PILING DATE: 1998-09-03 |
| PRIOR PILING DATE: 1998-05-13 |
| PRIOR PILING DATE: 1998-04-17 |
| NUMBER OF SEQ ID NOS: 49 |
| SOFTWARE FELING DATE: 1998-04-17 |
| NUMBER OF SEQ ID NOS: 49 |
| SOFTWARE PATENTIN VET. 2.0
                                                                                                                                  publication US/10218743

| Sequence 13, Application US/10218743
| Publication No. US203009677941
| GENERAL INFORMATION:
| APPLICATION NO. US2031009677941
| GENERAL INFORMATION:
| APPLICANT: Munter, Shirley Wu
| APPLICANT: Hunter, Shirley Wu
| APPLICANT: Weber, Eric R.
| TITLE OF INVENTION: NOUSE DEMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEING DATE: 1090-04-15
| PRIOR PRILING DATE: 1090-04-15
| PRIOR PLILING DATE: 1990-05-13
| PRIOR PLILING DATE: 1990-05-13
| PRIOR PLILING DATE: 1990-05-13
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| PRIOR PLILING DATE: PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAMENTER PARAME
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100.0%; Pred. No. 7.6e-09;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-13
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ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DPAKGMSPPGFIVGEEGVLS 20
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Matches 20; Conservative
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LENGTH: 490
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APPLICANT: MCGALL, Catherine A.
APPLICANT: MCGALL, Catherine A.
APPLICANT: MCGALL, Catherine A.
APPLICANT: MCGALL
APPLICANT: MCGALL
APPLICANT: MCGALL
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVER: US/09/29,225
PRIOR APPLICATION NUMBER: US/09/29,225
PRIOR FILING DATE: 1998-09-04-15
PRIOR FILING DATE: 1998-09-04-15
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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US-10-218-743-35

J Sequence 35, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: McCall, Catherine A.

APPLICANT: McDer, Eric R.

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3

CURRENT FILING DATE: 2002-08-13

FURRENT FILING DATE: 1999-04-15

PRIOR PLICATION NUMBER: 60/086,295

PRIOR PLICATION NUMBER: 60/086,295

PRIOR PLING DATE: 1998-04-17

PRIOR PLING DATE: 1998-04-17

PRIOR PLING DATE: 1998-04-17

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th 96.2%; Score 101; DB 14; Length 490; I Similarity 95.0%; Pred. No. 9.4e-07; 19; Conservative 0; Mismatches 1; Indels (
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Sequence 238601, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 Application US/10218743
| Sequence 18 Application US/10218743
| Sequence 18 Application US/10218743
| Publication No US20030096779A1
| GENERAL INFORMATION:
| APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu. APPLICANT: Weber, Eric R. TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFRENCE: AL-2-C3
| TITLE OF INVENTION: AND USES THEREOF FILE REFRENCE: AL-2-C3
| CURRENT APPLICATION NUMBER: US/10/218,743
| CURRENT FILING DATE: 1999-04-15
| PRIOR FILING DATE: 1999-04-15
| PRIOR FILING DATE: 1998-09-02
| PRIOR FILING DATE: 1998-09-05
| PRIOR FILING DATE: 1998-04-17
| PRIOR FILING DATE: 1998-04-17
| PRIOR FILING DATE: 1998-04-17
| PRIOR FILING DATE: 1998-04-17
| PRIOR FILING DATE: 1998-04-17
| NUMBER OF SEQ ID NOS: 49
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 18
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Pred. No. 2.1e-06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99; DB 14;
Pred. No. 2.1e-06;
0; Mismatches 1.
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR PILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 15
IENCHT: 555
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-10-218-743-15
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Best Local Similarity 95.0%;
Matches 19; Conservative
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| Sequence 31, Application US/10218743
| Sequence 31, Application No. US2030096779A1
| GENERAL INFORMATION:
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McDer, Eric R. |
| TITLE OF INVENTION: NOVEL DERWATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS |
| TITLE OF INVENTION: NOVEL DERWATOPHAGOIDES NUCLEIC ACID MOLECULES, PRICE REFERENCE: AL-2-C3 |
| CURRENT APPLICATION: NOWBER: US/10/2125 |
| PRIOR APPLICATION NUMBER: G0/098, 909 |
| PRIOR FILING DATE: 1998-09-13 |
| PRIOR PILING DATE: 1998-04-17 |
| PRIOR FILING DATE: 1998-04-17 |
| PRIOR FILING DATE: 1998-04-17 |
| NUMBER OF SEQ ID NOS: 49 |
| SEQ ID NO 21 |
| LENGTH CHANCE ACCORDANCE ACCO
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96.2%; Score 101; DB 14; Length 509;
Best Local Similarity 95.0%; Pred. No. 9.8e-07;
Matches 19; Conservative 0; Mismatches 1; Indels
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Pred. No. 2.1e-06;
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-21
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                                                                                                          TYPE: PRT ; ORGANISM: Dermatophagoides farinae US-10-218-743-38
                                                                                                                                                                                                                                                                                                                                                                                                      298 DPAKGMSPPGFITGEEGVLS 317
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Best Local Similarity 95.0%;
Matches 19; Conservative
            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 509
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Sequence 6, Application US/10067615
Publication No. US20020115154A1
| GENERAL INFORMATION:
| APPLICANT: Alnemi, Emad S. | TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND | TITLE OF INVENTION: NETHODS OF USE THEREOF | TITLE OF INVENTION: NETHODS OF USE THEREOF | TITLE OF INVENTION: NUMBER: US/10/067,615 | CURRENT FILING DATE: 2002-02-04 | NUMBER OF SEQ ID NOS: 6 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NOS: 6 | CORRENT SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | TENCH SECOND | T
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TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 480140.432D3
CURRENT APPLICATION NUMBER: US/10/076,754
CURRENT PILING DATE: 2002-02-12
SUPPLES OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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43.8%; Pred. No. 55;
tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 13; Length 350;
Pred. No. 55;
                                                                                     Score 48; DB 9; Length 57;
Pred. No. 7.8;
4; Mismatches 2; Indels
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Publication No. US20020161196A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10076754 Publication No. US20020161195A1 GENERAL INFORMATION:
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                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                         6 MSPPGFIVGEEGVL 19
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Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
         ; ORGANISM: Homo sapiens
US-09-925-302-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-076-773-6
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 181344
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 238601
LENGTH: 143
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Sequence 483, Application US/09925302

Sequence 483, Application US/09925302

BAPLICARY: Rosen et al.

APPLICARY: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: DC1/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 483

LENGTH: ST
                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 12; Length 143;
Pred. No. 11;
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Pred. No. 6.8;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_134769C.1.pep
                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_57482C.1.pep
US-10-424-599-238601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PNKGEDPPKFFNVVGEEG 138
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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US-10-424-599-181344
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US-09-925-302-483
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Matches
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE OF THYENTON: METHODS OF USE THEREOF FILE REPERENCE: 480140.43202 CURRENT APPLICATION NUMBER: US/10/076,773 CURRENT FILING DATE: 2002-02-12 NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 350
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-773-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Best Local Similarity 43.8%; Pred. No. 55;
Matches 7; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08916625B
; Bollication No. US2010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KETTH C.
APPLICANT: YOUNG, PETER R.
ITILE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
ITILE OF INVENTION: RECEPTOR, TR6
CORRESPONDENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 10
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDLUM TRYE: DAS CHECK
COMPUTER READABLE FORM:
MEDLUM TRYE: DAS CHECK
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COMPUTER READABLE FORM:
MEDLUM TRYE: DAS CHECK
COMPUTER READABLE FORM:
MEDLUM TRYE: DAS CHECK
FILING DATE: 22-AUG-1997
CLASSIFICATION NUMBER: 06/041,230
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
TELERACOMENT AND CHECK
MODECULE TYPE: Amino acide
STRANDENES: BASES
INDEMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 411 amino acide
STRANDENES: BIOLE
MODECULE TYPE: Amino acide
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76 PSEGLCPPGHHISEDG 91
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Score 48; DB 8; Length 411; Pred. No. 65;

45.7%;

Query Match Best Local Similarity

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 protein search, using sw model OM protein Run on:

March 22, 2004, 06:42:54 ; Search time 1.61201 Seconds (without alignments) 640.518 Million cell updates/sec

Title: Perfect score:

US-09-662-293-13 105 1 DPAKGMSPPGFIVGEEGVLS 20

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /ogn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /ogn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /ogn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /ogn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	4, Appli	13, Appl					15, Appl		6, Appli	2, Appli	1, Appli	2, Appli	3, Appli				2, Appli		24263, A	30682, A		34, Appl		18602, A	5334, Ap	28,	4952, Ap
Description	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
Δī	-292-22	US-09-292-225-13	US-09-292-225-41	09-292-22	US-09-292-225-38	39-29	US-09-292-225-15	-09-292-	09-134-61	-63	-04-019-	-618-	-10-039-7	ç	-09-333-	-08-883-	US-09-536-201-2	-09-578-	US-09-252-991A-24263	US-09-252-991A-30682	US-09-252-991A-20817	-08-705-660-3	US-08-989-045-34	-09-252-991A	-09-543-681A-53	-19	US-09-134-000C-4952
BB	4	4	4	4	4	4,	4,	4	4,	ო	4	4	4	4	4	m	4	4	4	4	4	7	m	4	4	4	4
Length	20	20	490	509	509	536	555	555	350	411	411	411	411	412	424	440	440	440	420	503	219	3224	3224	411	915	367	385
% Query Match	100.0	100.0	96.2				94.3	94.3	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	44.8	42.9	41.9	•	41.9	•	ο.	39.0	39.0
Score							66	66	48	48	48	48	48	48	4.8	48	48	48	47	45	44	44	44	42	41.5	41	41
Result No.		2	ო	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 21851, A	5516,	115	H		Sequence 458, App	Sequence 17298, A	554	Sequence 3, Appli	Sequence 3, Appli	544	Sequence 6, Appli	Sequence 32847, A	Sequence 26412, A	Sequence 53, Appl	Sequence 6265, Ap	Sequence 21650, A
US-09-252-991A-21851	90	US-09-489-039A-11591	US-08-821-119-17	US-08-821-118-5	US-09-198-452A-458	US-09-252-991A-17298	US-09-328-352-5542	US-08-459-146-3	US-08-459-065-3	US-09-543-681A-5442	US-09-043-627-6	US-09-252-991A-32847	US-09-252-991A-26412	US-08-401-512-53	US-09-107-532A-6265	US-09-252-991A-21650
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433	456	519	611	611	845	1049	1596	3165	3165	72	366	484	509	54	61	280
39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	38.6	38.6	38.6	38.6	38.1	38.1	38.1
4,	† 4 *	41	41	41	41	41	41	41	41	40.5	40.5	40.5	40.5	40	40	40
58	N 60	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-90-644-62-4

Dequence 4, Application US/0929225

Patent No. 6455886

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Macall, Catherine A.
APPLICANT: Meber, Eric R.
TITLE OF INVENTION: NOUSES THEREOF
FILE REFERENCE: AL-2-C3
FURREY PELLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
FARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
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EARLIER APPLICATION NUMBER: 09/662,013
EARLIER APPLICATION NUMBER: 09/662,013
EARLIER PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
LENGTH: DATE: 1005-10062,013
EARLIER PILING DATE: 1998-04-17
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Patent No. 6455686
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Muter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: AL.2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
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Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Dermatophagoides farinae US-09-292-225-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DPAKGMSPPGFIVGEEGVLS 20
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JS-09-292-225-4
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APPLICANT: Weber, Eric R.

ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT PAPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER PILING DATE: 1998-04-17
SARLIER PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN OF: 2.0
SEQ ID NO 38
LENGTH: 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 4; Length 509;
Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                           Sequence 21, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
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INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/0929225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunner, Shirley Wu
APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 DPAKGMSPPGFITGEEGVLS 317
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1 Similarity 95.0%;
19; Conservative
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Matches 19; Conserva
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Matches 19; Conserv
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US-09-292-225-21
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US-09-225-41
Sequence 41, Application US/0929225
Sequence 41, Application US/0929225
Sequence 41, Application US/0929225
Sequence 41, Application US/0929225
Sequence 41, Application C45566
GENERAL INFORMATION:
APPLICANT: Weber, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
SEARLIER FILING DATE: 1998-04-15
EARLIER APPLICATION NUMBER: 60/098, 909
EARLIER APPLICATION NUMBER: 60/098, 565
EARLIER APPLICATION NUMBER: 60/098, 565
EARLIER PILING DATE: 1998-04-17
SEARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEGURANE: PATENTING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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Sequence 35, Application US/09292225

Sequence 35, Application US/09292225

Sequence 35, Application US/09292225

SEGNERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: Mcber, Shirley Wu

APPLICANT: Weber, Exic R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 105; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 20; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
SARLIER PARTIER PARTIER DATE: 1998-04-17
SARLIER PARTIER PARTIER DATE: 1998-04-17
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SARLIER PARTIER PARTIER DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Dermatophagoides farinae US-09-292-225-13
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LENGTH: 490
TYPE: PRT
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APPLICANT: McCall, Catherine A.
APPLICANT: McCall,
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Henter, Shirley Wu
APPLICANT: Henter, Shirley Wu
APPLICANT: Henter, Shirley Wu
APPLICANT: Weber,
FILLE OF INVENTION: AND USES THEREOF
FILLE REPERENCE: AL-2-C3
FILLE REPERENCE: AL-2-C3
FILLE REPERENCE: AL-2-C3
FILLE APPLICATION NUMBER: G0/099,909
FARLIER APPLICATION NUMBER: G0/099,909
FARLIER APPLICATION NUMBER: G0/099,525
FARLIER APPLICATION NUMBER: G0/099,565
FARLIER PILING DATE: 1998-04-17
FARLIER FILLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SECTIMARE: PATENTIN NUMBER: G0/062,013
FARLIER FILLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEG ID NO 18
LENGTH: 555
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Sequence 6, Application US/09134618

Patent No. 6417328

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REPREMENT: 849410.432.

CURRENT APPLICATION NUMBER: US/09/134,618

CURRENT PILING DATE: 1999-08-14

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 6

LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 6.7;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.3%; Score 99; DB 4; Length 555; Best Local Similarity 95.0%; Pred. No. 6.6e-08; Matches 19; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Dermatophagoides farinae
US-09-292-225-18
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APPLICANT: Chutcharapai, Anan
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METEOD FOR
TITLE OF INVENTION: CROSS-REAC
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Best Local Similarity 43.8
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-09-134-618-6
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US-09-29-225-15

Sequence 15, Application US/0929225

Patent No. 6455686

GENERAL INFORMATION:

APPLICANT: Macall, Catherine A.

APPLICANT: Macall, Catherine A.

APPLICANT: Macall, Catherine A.

APPLICANT: Maber, Exic R.

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHACOIDES NUCLEIC ACID MOLECULES, PROTEINS

TATLIER APPLICATION NUMBER: GO/098, 909

EARLIER FILING DATE: 1998-09-13

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-04-17

SEQ ID NO 15

LENGTH: 555

TAYBE: DERMATES

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                       APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER PLING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER: 05 FILING DATE: 1998-04-17
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NUMBER: 05 FILING DATE: 1098-04-17
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US-09-292-225-18
; Sequence 18, Application US/09292225

// TYPE: PRT
// ORGANISM: Dermatophagoides farinae
US-09-292-225-21

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US-09-292-225-15
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Best Local Similarity 95.0%;
Matches 19; Conservative
Hunter, Shirley Wu
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Sequence 2, Application US/09134618

Sequence 2, Application US/09134618

Sequence 2, Application US/09134618

GENERAL INFORMATION:
APPLICANT' ADIGNT', Emad S.
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPRENCE: 480140.432

FULLE REPRENCE: 480140.432

CURRENT APPLICATION NUMBER: US/09/134,618

CURRENT FILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 2

LENTH: 411
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WESULT IN 0. 653838

FREEDER No. 653838

FREEDER No. 653838

FRIERRAL INPORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS50

CURRENT APPLICATION NUMBER: 60/34,037

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR PILING DATE: 2001-11-4

PRIOR PILING DATE: 2001-11-4

PRIOR APPLICATION NUMBER: 60/323,807

PRIOR PILING DATE: 2001-10-09

FRIOR APPLICATION NUMBER: 60/329,807

PRIOR PILING DATE: 2001-00-01

PRIOR APPLICATION NUMBER: 60/329,473

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-04

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43.8%; Pred. No. 8;
tive 5; Mismatches 4; Indels
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43.8%; Pred. No. 8;
ive 5; Mismatches 4; Indels
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76 PSEGLCPPGHHISEDG 91
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Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
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US-10-039-785-3
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ORGANISM: Homo sapiens
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Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels
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45.7%; Score 48; DB 4; Length 411;
Best Local Similarity 43.8%; Pred. No. 8;
Matches 7; Conservative 5; Mismatches 4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
FILE REFERENCE: P1468R1 (REVISED)
CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1999-06-10
FRIOR APPLICATION NUMBER: US 60/089,253
FRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
SEQ ID NO 2
TENGTH: 411
TYPE: PRT
CRANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09079029; Patent No. 6342369; GENERAL INFORMATION: APPLICANT: Adams, Camilia W. APPLICANT: Ashkenazi, Avi J. APPLICANT: Chuntharapai, Anan APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: xaa
LOCATION: 410
CTHER INFORMATION: xaa = leu oz met
US-09-329-633A-2
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NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
CITY: South San Francisco STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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76 PSEGLCPPGHHISEDG 91
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US-09-079-029-1
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76 PSEGLCPPGHHISEDG 91

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45.7%; Score 48; DB 4; Length 424;

Query Match

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Best Local Similarity 43.8%; Pred. No. 8.3;

Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPPGFIVGEG 17

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Db 76 PSEGLCPPGHHISEDG 91

Search completed: March 22, 2004, 07:03:57

Job time: 1.61201 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 22, 2004, 06:40:28; Search time 36.0951 Seconds (without alignments) 1479.047 Million cell updates/sec Run on:

US-09-662-293-15 3107 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

· m	Description	(EC 3	e (EC 3		chitinase (EC 3.2.	hypothetical prote	oviduct-specific g	estrogen dependent	oviductal glycopro	cartilage glycopro	heparin-binding gl	breast-regressing	secretory protein	chitinase (EC 3.2.		chitinase (EC 3.2.	chitinase A [impor	chitinase (EC 3.2.	hypothetical prote	chitinase (EC 3.2.	chitinase VCA0027	hypothetical prote	chitinase precurso	chitinase B homolo	e e	н	chitinase - fungus	m	tinase	chitinase (importe
SUMMARIES	ΩĪ	T44445	T14075	A56596	A53918	T15408	S57197	54	138605	A49562	851327	861551	S27879	A38221	D83764	A38368	T43916	T00323	T29275	T44440	D82510	T03884	860651	AB1452	JQ1975	S68121	S51369	AB1088	A25090	F84238
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-	Length	525	1635	554	483	617	537	539	654	383	383	405	399	504	599	669	1215	831	1484	869	849	2025	563	756	423	424	423	756	561	546
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JC4038	T24898	T30418	\$47133	A40633	PC4106	T20950	T35719	T10393	T04761	D82246	S61166	T04762	T41863	G72865	JC4565
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394	394	391.5	389	388	385	382	379.5	377.5	371.5	369	367.5	365	364.5	360.5	359.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PITTPITTIPITTPITTPSPITTPSPITTPSPITTPSPITTPSPITTPTTPSPITTPTTPTTPTTST 481
APTT----STVAPGTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG 466
                                                                                                                                                      500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-1635 <DEL>
; Cross-references: EMBL:AF026492; NID:92564720; PID:92564721; PIDN:AAB81850.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECIL--GPSTTTPT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 YKYTIQVFDPYQDDNHNSW---EKRGYERFNNLRLKNPELITMISLGGWYEGS-EKYSDM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPK----IDKQNYLALVRELKD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                    Chitinase (EC 3.2.1.14) - yellow fever mosquito
Chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14075
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosop
A;Reference number: Z17872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSPTTTEHTSETPKY------TTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IKRDHNDYSKNPM-----RIVCYVGTWSVYHKVD-PYTIEDIDPPKCTHLMYGFAKIDE
                                                                                          TTTEHTSETPKYTTYVDGHLIKCY --KEGDIPHPTNIHKYLVC-----EFVNGGWWVH
                                                                                                                                                      ------bg---bgaggryervehetwcaryrichtadtyreft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.0%; Score 869; DB 2; Length 16
34.3%; Pred. No. 4.8e-46;
tive 95; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T14075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- COEKLT 551
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---CPPGTLF 507
                                                                                                                                                                                                                 536 IMPCPPGTIW 545
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                                     414
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C;Species: Manduca sexta (tobacco hornworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
C;Accession: A56596
R;Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
Insect Biochem, Mol. Biol. 23, 691-701, 1993
A;Title: Sequence of a cDNA and expression of the gene encoding epidermal and A;Reference number: A56596
A;Accession: A56596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VDGSEI 497
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chitinase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
C;Species: Chelonus sp.
C;Species: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIPITIPSPIT ------PIP-TIPIPAPITSIPSPITIBHISBIPKYTIYVDGHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;NOČE: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
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                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-554 <KRA>
A;Cross-references: GB:U02270; GB:S64757; NID:g406048; PID:g406049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.0%; Score 838.5; DB 2; 35.4%; Pred. No. 9.2e-45; tive 79; Mismatches 210;
----LCPGGLYWSVDHCDWPQSTNCRNKQT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.4
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: mRNA
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387 405 429 458 449

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R; Sendai, Y; Abe, H; Kikuchi, M.; Satoh, T.; Hoshi, H.
Biol. Reprod. 50, 927-934, 1994
A; Title: Purification and molecular cloning of bovine oviduct-specific glycoprotein.
A; Reference number: 857197; MUID:94257768; PMID:8199272
A; Accession: 857197
A; Accession: 857187
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-537 < SEN>
A; Cross-references: EMBL:D16639; NID:g391621; PIDN:BAA04065.1; PID:d1004583; PID:g391622
C; Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 TMLSTFSNRERFVSSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWTFVFLLEELLQAF 164
                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                               346
CYFTNWAQYRQGRAKFVPEDYTPGICTHILFAFGWMA-DYTVRAYDP--ADLFNDWAGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oviduct-specific glycoprotein 95% precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Accession: 857197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS
                                                                                     229 GYDIPNLAPNFDFILLMSYDFFGAWASLVGFNSPLYATTELPAEWNGW-NVDSSARYWNQ
                                                                                                                                                                                                                                                                                                                               288 KGMPKEKIIVGMPTYGRGWTLNNASAINPGTSGSPAKITQYVQ-EAGVGAYFEFCEMLAN
                                                                                                                                                                                                                           AYDI KELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN
                                                                                                                                                                                                                                                                                                          268 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK
                                                                                                                                                                                                                                                                                                                                                                                         328 EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNSNGQLYPLISVIAKELGG-----VIIPKKGGVTTAPTTVATTVTTGRPPMTSAVTT
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                                                              G-YERFINILRIKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLQEYKFDG
                                                                                                                                          LDLDWEYPGSRLGNPKIDKONYLALVRELKDAPEPHG-----YLLTAAVSPGKDKIDR
                                                                                                                                                                                                                                                                                                                                                                                                                            347 GATR-YWDSQSQVPYLVQGNQWWSYDDEESFANKWAYVKREGYGGAFVWTLDFDDFNAGC
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  C,Accession: A53918
R;Krishnan, A.; Nair, P.N.; Jones, D.
A;Krishnan, A.; Nair, P.N.; Jones, D.
J. Biol. Chem. 269, 20971-20976, 1994
A;Title: Isolation, cloning, and characterization of new chitinase stored in active f
A;Reference number: A53918; MVID:94342256; PMID:8063715
A;Accession: A53918; MVID:94342256; PMID:8063715
A;Accession: A53918
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;References: CB:U10422; NID:9533504; PIDN:AAA61639.1; PID:9533505
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C04F6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15408
R;Nhan, M.
Submitted to the EMBL Data Library, December 1995
A;Reference number: 218346
A;Reference number: 218346
A;Reference number: 218346
A;Residues: T15408
A;Residues: 1-617 < NHA>
A;Residues: 1-617 < NHA>
A;Residues: 1-617 < NHA>
A;Cross references: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CE
C;Genetics: 28/1; 66/2; 504/1
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                                                                                                                                                                                                                                              Query Match 25.8%; Score 802; DB 2; Length 483; Best Local Similarity 36.1%; Pred. No. 1.4e-42; Matches 160; Conservative 89; Mismatches 162; Indels
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NiAlternate names: 39K symovial protein
C:Species: Homo sapiens (man)
C:Species: Amar-1995 #sequence_revision 23-Mar-1995 #text_change 22-Jun-1999
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                      -TITPSPTTPTTTPSPT
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                                                                         390 TPSPKFWFSTAVNSSRIGPEMPTMTRDLTTGLGILPLGGEAVATETHRKSATMTTTPRGE
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Matches 176; Conservative 9
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C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change O5-Nov-1999
C,Grossion. M. M. Murray, M.K.
Endocrinology 136, 2485-2496, 1995
A,Title: An estrogen-dependent secretory protein, which shares identity with chitinases, and embryo development.
A,Reference number: 146470, MUID:95269691; PMID:7750470
A,Accession: 146470
A,Accession: 146470
A,Accession: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-539 <DES>
A,Residues: 1-539 <DES>
A,Cross-references: EMBL:U16719; NID:g885600; PIDN:AAC48471.1; PID:g885601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSXLKLGDPA 300
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                                                                                                        300
                                                                                                                                       TPSPKFWFSTAVNSSRIGPEMPTWTRDLTTGLGILPPGGEAVATETHRKSETWTITPKGE 446
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                                                                                                                                                                                                                   KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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                              EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
                                                                                                        PLYKRPDETDELHTYPNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
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Pred. No. 3.2e-35;
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33.8%;
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S61551; S61550; T48271
R;Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A;Title: new and ras initiate murine mammary tumors that share genetic markers ge
A;ATitle: new and ras initiate murine mammary tumors that share genetic markers ge
A;Attle: andleic acid sequence not shown
A;Reference number: 1405 cMOR1>
A;Residues: 1-405 cMOR1>
A;Residues: 1-405 cMOR1>
A;Residues: 1-405 cMOR1>
A;Residues: 1-405 cMOR1>
A;Residues: Leferences: EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; PID:g1085066
R;Morrison, B.W.
S;Dmitted to the EMBL Data Library, November 1995
A;Reference number: S61550
A;Reference number: S61550
A;Reference number: mounty at the muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three muscular and a three mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 LQGAT--VRRPLGQQVPYATKGNQWVGYDDQESVRNKAKYLKSRQLAGAMVWTLDLDDFR 360
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A,Molecule type: mRNA
A,Residues: 1-245, "12, 247-330, "H', 332-350, "MVWALDLDDFQGTCQPKEFFPLTNAIKDALA' <
A,Cross-references: EMBL:X93035; NID:g1.085065; PIDN:CAA63603.1; PID:g1085066
A,Note: the differences at the carboxyl end are due to a frameshift error
                                                                                                                                                                                                                                                   92 W-EKRGYERFINILRIKNPELTIMISLGGWYEGSEKYSDMAANPIYRQQFIQSVLDFLQEY
                                                                                                                                                                                                                                                                                         265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 VLRIGAPANKLVMGIPTFGRSFTLAS-SKTDVGAPASGPGIPGRFTKEKGILAYYEICDF
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1-21/Domain: signal seguence #status predicted <SIG>
122-405/Product: breast-regressing protein brp39 #status predicted
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              36.6%; Pred. No. 3.1e-33;
Live 77; Mismatches 130;
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              Local Similarity 36.6
nes 139; Conservative
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S1327
R;Shackelton, L.M.; Mann, D.M.; Millis, A.J.T.
Submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in differe
                                                                                                                                                                                                                                                                                                                                                                                                                            similar to a bovine mammary prote
                                                                                                                    and
                                                                                                                articular chondrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRG---YERFINNLRLKNPELTTMISLG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALVRELKDAF----EP--HGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVWTYDYHGG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 WENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTGFVVLVLLQCC------SAYKLVCYYTSWSQYREGDGSCFPDALDRFL 50
C;Accession: A49562; S10677; A33162
R; Hakala, B.E.; White, C.; Recklies, A.D.
J. Biol. Chem. 268, 25803-25810, 1993
A; Title: Human cartilage gp-39, a major secretory product of articular chondra A; Reference number: A49562; MUID:94064658; PMID:8245017
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A49562
A;Accession: A269, A265-268, 1990
Biochem. J 269, A265-268, 1990
A;Title: Human synovial cells secrete a 39 kDa protein similar to a bovine ma A;Reference number: S10677; MUID:90328983; PMID:2375755
A;Accession: S10677; MUID:90328983; PMID:2375755
A;Accession: S10677
A;Wolecule type: protein
A;Residues: 22-40, X', 42-45 < ANY2>
C;Supportamily: Streptomyces chitinase chi40
C;Gsuporfamily: Streptomyces extracellular protein; glycoprotein
F;1-21/Domain: signal sequence #status predicted <AMT>
F;22-383/Product: cartilage glycoprotein gp39 #status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIED-IDPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SNDHIDTWEWNDVTLYGMLNTLKONRNPNLKTLLSVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.3%; Score 662; DB 2; Length 38 34.9%; Pred. No. 5.5e-34; rive 81; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z47803; NID:g634097; C;Superfamily: Streptomyces chitinase chi40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Siminary,
Matches 144; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-383 <SHA>
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셤 8 ద Š 임 8 ద ò 요 ⋧ 9 8 유 Length 383;

5 DB

Score 650;

20.9%;

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Chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83764
B;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Recession: D83764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-599 <STO>
A;Residues: 1-599 <STO>
A;Residues: 1-599 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04635.1; GSPDB:GN001
                                                                                                                                                   brugian
           C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Brugia malayi
C.Species: Or.Nar1: 933 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C.Accession: A38221
R.Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Narl: Acad. Sci. U.S.A. 89, 1548-1552, 1992
A.Title: Transmission-blocking antibodies recognize microfilarial chitinase in brugi
A.Reference number: A38221; MUID:92179220; PMID:1542646
A.Accession: A38221
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: nucleic acid; protein
A.Molecule type: nucleic acid; protein
A.Residues: 1-504 *FUH>
A.Cross-references: GB:M73689; NID:9156063; PIDN:AAA27854.1; PID:9156064
A.Noce: sequence extracted from NCBI backbone (NCBIP:85345)
C.Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 FDLDWEYPVGVAEEHAKLVEAMKTAFVEEAKTSGKQR-LLLIJAAVSAGKGTIDGSYNVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 INKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 KLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 YDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 RGYERFINNIRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 LDLDWEYP-GSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 TTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY-----VDGHLIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 CYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQ-DDNHNSWEK
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                                                                                                                                                                                                                                                                                                                                                                             ; Score 604.5; DB 2;
; Pred. No. 3e-30;
86; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                             19.5%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 30.1%
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secretory protein YM-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 22-Jun-1999
C;Accession: 827879
C;Accession: 827879
R;Chang, N.C.A.; Liu, C.H.; Chang, A.C.
submitted to the EMBL Data Library, June 1992
R;Chestion: Molecular characterization of a secretory protein (YM-1) transiently expr
A;Residue: 827879
A;Molecule type: mRNA
A;Residue: 1-399 CCHA>
A;Molecule type: mRNA
A;Residue: 1-399 CCHA>
A;Cross-references: EMBL:M94584; NID:g202441; PIDN:AAB62394.1; PID:g202442
C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <NAT>
F;22-399/Product: secretory protein YM-1 #status predicted <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIISYWKDHGAASEKLIVGFPAYGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYY 305
                                                                                                            185 AIDTGYDIAQIAQHLDFINLMTYDFHGVWRQITGHHSPLFQGQXDT-RFDRYSNVNYAVQ 243
                                                                                                                                                                            323
                                                                                                                                                                                                   244 YMTRIGAQASKLIMGIPTFGKSFTLAS-SENQIGAPISGEGLPGRFTKEAGTLAYYEICD 302
                                                                                                                                                                                                                                                                                          SWEKRGYERFINNLR-LKNPELLTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQE 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELCQLFQK---BEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVW 376
203
                                           184
                                                                                       263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVCTFLNEGATEVW----DAPQEVPYAYQGNEWVGYDNVRSFKLKAQWLKDNNLGGAVVW 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EP--HGYLLTAAVSPGKD
                                         131 YGFDGLDLAWLYPRLR-----DKQYFSTLIKELNAEFTKEVQFGREKLLLSAALSAGKV
                                                                                  KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETHTYFNVNYTMH
                                                                                                                                                                            YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCO
                                                                                                                                                                                                                                                                   324 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGV-----MVWSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKI--DEYKYTIQVFDPYQDDNHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                    ----SGHCQPXN-------38RSPTPSRMP 378
                                                                                                                                                                                                                                                                                                                                                           NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.6%; Score 608; DB 2; Length 399; 36.3%; Pred. No. 1.3e-30; rative 67; Mismatches 140; Indels
YKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF
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PLDMDDFSGSFCHQRHFPLTSTLKGDLN 389
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RESULT

23;

Gaps

156;

Indels

67; Mismatches 185;

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GWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYKFDGLDLDWEYP--GSRLGNPK--IDK 173
                                                                                                                                                                                                                                                                                                                                                          YHGGWENFYGHNAPLYKRPDET----DELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | | | : | | | : | 340 RGWDGCAQAGNGQYQTCTGGSSVG--TWEAGSFDFYDL-----EANYINKNGYTRYWND 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 ---APYGYN--DKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 ASTDNVGVTGYNVYNGANLATSVTGTTATISGLTAGTSYTFTIKAKDAAGNLSAASNAVT
                                                                 QNYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 TAKVPYLYNASNKRFISYDDAESVGYKTAYIKSKGLGGAMFWELSGDRNK------
                                                                                                                    DEYKYTIOV-----PDPYQDDNH----NSWEK---RGYERFNNLRLKNPELTTMISLG
                                                                                                                                                                                                                                                                                                                                                                                                                                        RAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQ---YDEYYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 NKVHNMINGDEKNSFECILGPSTTTPTPTTTTTTTTTTTT-----
                                      34 RIVCYVGTWSVYHKVDPYTIEDIDPPKCTHLMYGFAKI-
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he : 37.0951 secs
  170; Conservative
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A38368
chitinese (EC 3.2.1.14) precursor - Bacillus circulans
C.Species: Bacillus circulans
C.Species: Bacillus circulans
C.Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 15-Oct-1999
C.Accession: A38368
R.Hatle: Gene cloning of chitinase Al from Bacillus circulans H.
J. Biol. Chem. 265, 15659-15665, 1990
A.Title: Gene cloning of chitinase Al from Bacillus circulans WL-12 revealed its evoluti
A.Reference_number: A38368; MJID:90368776; PMID:2203782
A.Reference_number: A38368; MJID:90368776; PMID:2203782
A.Relaus: preliminary
A.Molecule type: DNA
A.Residues: 1-699 < MAD-
A.Cross-references: GB:M57601; GB:J05599; NID:g1066341; PIDN:AAA81528.1; PID:g142688
C.Superfamily: fibronectin type III repeat homology
C.Reywords: glycosidase; bydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                              :|: | | | |
67 SHINYAFANICWDGRHGNPDFAGPNPQTWSCQDENGVIDVPNGSIVMGDPWIDAQKSNPG 126
                                                                                                                                                                                                                                                                                                                                                                                                                         IRKYGFDGVDVDWEYPVSGGLPGNSRRPEDKENHVLLLQEVRDKLDEAGQEDGKDYLLTI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A--vspgkdkidraydikelnklfdwmnvmTydyHGGWenfyGHNAPLyKRPDETD-ELH 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 ASGASPGYVENNK---LNEIAEIVDWINIMTYDFNGGWQNISGHNAPLYYDPATANTELP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPEHFNVESAVEGHLOAGVPEHKLVLGMPFYGRGWSNCDGA--NQGEYOR-CAPPREGTW 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 AFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTP 422
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                                                                                                                                                                                                                                                                                                                     90 NSWEK--RG-YERFNNLRLKNPELTTMISLGGWYEGSEKYSDWAANPTYRQQFIQSVLDF 146
                                                                                                                                                                                                                                                                                                                                                                                                   147 LQEYKFDGLDLDWEYP--GSRLGNPK--IDKQNYLALVRELKDAFEPHG-----YLLTA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T - - YFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PETTYTEVVSAEHKDGIRHAGQALQVTTKSETGGDGCTAPTWQANNVYTGGDQVQHGGKL 571
                                                                                                                                                                                                 99
                                                                                                                                                                                                                                        ----IDEYKYTIQVFDPYQD----DNH 89
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                                                                                                                                                                                 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPPKC
                                                                                                                    Gaps
                                                                             19.1%; Score 592; DB 2; Length 599;
29.0%; Pred. No. 2.3e-29;
ive 98; Mismatches 216; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKYLVCEFVNGGWWVHIMPCPPGT----IW 545
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                                                                                                                                                                                                                                        THIMYGFAK------
A, Experimental source: strain C-125 C, Genetics: A, Gene: BH0916
                                                                             Ouery Match
Best Local Similarity 29.0°
Matches 183; Conservative
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PITITESP - - TIPITITIPIP-APITSIPSPITIEHISET 493
                                                                                     547 VSTTAQPGGDTQAPTAPTNLASTAQTTSSITLSWTAST 584
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Length 699;

Score 561; DB 2; Pred. No. 2.3e-27;

18.18;

Query Match Best Local Similarity

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 22, 2004, 06:31:13; Search time 21.2868 Seconds (without alignments) 1357.597 Million cell updates/sec Run on:

US-09-662-293-15 3107 1 MKTIYAILSIMACIGLMNAS......IMPCPPGTIWQGKLTCIGE 555

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q62635 rattus norv	COSO49 Xenopus rae	Ol0341 orgyia pseu	P10667 xenopus lae	P22533 caldocellum	P14918 zea mays (m	Q06885 dictyosteli	P47179 saccharomyc	P22699 dictyosteli	P09805 kluyveromyc	P24152 sorghum bic	P02840 drosophila
MUC2 RAT	MUC1_XENLA	Y091_NPVOP	MUA1 XENLA	MANB_CALSA	EXTN_MAIZE	GP10_DICDI	DAN4 YEAST	GUN6_DICDI	KTXA_KLULA	EXTN SORBI	SGS3_DROME
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-	7.9	7.7	7.4	7.3	7.1	7.0	7.0	6.9	6.9	6.7	6.7

ALIGNMENTS

Euteleostomi;

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Fusetti F., von Moeller H., Houston D., Rozeboom H.J., Dijkstra B.W., Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;
"Structure of human chitotriosidase. Implications for specific inhibitor design and function of mammalian chitinase-like lectins.";
J. Biol. Chem. 277:25537-25544 (2002).
-!- FUNCTION: Degrades chitin and chitotriose. May participate in the defense against nematodes and other pathogens. Isoform 3 has no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzymatic activity.
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-| SUBDUIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted. A small proportion is lysosomal.
-!- ALTERNATIVE PRODUCTS:
                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                 SEQUENCE OF 22-42 AND 178-198, FUNCTION, AND TISSUE SPECIFICITY MEDLINE-95138187; PubMed=7836450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-386 IN COMPLEX WITH CHITOBIOSE AND ALLOSAMIDIN.
MEDLINE=22095530; Pubmed=11960986;
                                                                                                                                                                                                                                                                                                             "Purification and characterization of human chitotriosidase, a member of the chitinase family of proteins."; J. Biol. Chem. 270:2198-2202(1995).
                                                                                                                                                                                    Cloning of a cDNA encoding chitotriosidase, a human chitinase
                                                                                                                                                                                                                                                                          Renkema G.H., Boot R.G., Muljsers A.O., Donker-Koopman W.E.,
Aerts J.M.F.G.;
                                                                                                                                                                                                                                                                                                                                                                          POLYMORPHISM, AND DESCRIPTION OF ISOFORM 3.
MEDLINE=98421482; PubMed=9748235;
Boot R.G., Fenkema G.H., Verhoek M., Strijland A., Bliek J.,
de Meulemeester T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G.,
"The human chitotriosidase gene. Nature of inherited enzyme
                                                                                                                       TISSUB=Macrophage;
MEDLINE=96064695; PubMed=7592832;
Boot R.G., Renkema G.H., Strijland A., van Zonneveld A.J.,
                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                      produced by macrophages.";
J. Biol. Chem. 270:26252-26256 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 273:25680-25685(1998)
                 Homo sapiens (Human)
                                                                                                                                                                      Aerts J.M.F.G.;
                                                              NCBI_TaxID=9606
 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 -----SYTVPPPHTENTTPTPEWARPSTPSDPSEGDPIPTTTAKPASTTKTTVKTT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                           MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 KYSHMVAQKSTRMSFİRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 LYKRPHD-OWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 FECILGESTITFIPITFITFITET -----TIPTIPS-----PITFITFIFF 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE-------VDGSEI 497
                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 WYGYEDPRSVEIKWANIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKKILHKHMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL
                                                                                                                                                                                                                                                                                                                                                                                                           3 ATLATLAVLALATAV------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIPTITISPIT ------PIP-TIPIPAPITISTPSPITIEHISETPKYTIYVDGHLI
                                                                                                                                                                                                                                                                                                             ; Score 838.5; DB 1; Length 554;
; Pred. No. 6.3e-39;
79; Mismatches 210; Indels 91; Gaps
              Pfam; PF00704; GlyCo_hydro 18; 1.
SMART; SM00494; CheBD2, 1, GlyCo_hydro_18; 1.
SMART; SM00636; GlyCo_18; 1.
SMART; SM00636; GlyCo_18; 1.
SMART; ESSO944; CHIT BIND_11; 1.
PROSITE; PS01095; CHITIBIND_11; 1.
PROSITE; PS01095; CHITIBINE 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED------
                                                                                                                                                     ENDOCHITINASE.
SER/THR.RICH.
CHITIN-BINDING TYPE-2.
ENOTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CNSDODYIPDKKHCDKYWRC--VNGE--AMOFSCOHGTVFNVELNVC 540
                                                                                                                                                                                                                                                                                62203 MW;
                                                                                                                                                                                                                                                                                                                27.0%;
                                                                                                                                                                                                                                                                                                                               35.4%;
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 35.4<sup>3</sup>
Matches 208; Conservative
 Pfam; PF01607; CBM_14; 1
                                                                                                                                         545 :
554 AA;
                                                                                                                          Glycoprotein.
SIGNAL
                                                                                                                                                                                      DOMAIN
ACT SITE
CARBOHYD
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                       DOMAIN
                                                                                                                                                         CHAIN
d
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novel

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Note=Duplication of 24 bp in exon 10 leads to the use of a cryptic splice site. The normal splice site is still present but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macrophages.

DOLYMORPHISM: A 24 bp duplication in exon 10 leads to the activation of an alternative splice site and the production of an alternative splice site and the production of an inactive protein. About 6% of the population are deficient for CHIT1 activity, while 35% are carriers and show reduced enzyme levels. People with CHIT1 deficiency appear perfectly healthy.

MISCELLANGOUS: Patients with type 1 Gaucher disease (GD I)

[MIM:230800] have very high plasma levels of CHIT1, and this can be used as diagnostic aid and to evaluate the success of treatment. Successful therapy brings the CHIT1 activity levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Detected in spleen. Secreted by cultured
                                                                                                                                                                      IsoId=Q13231-2; Sequence=VSP_008631, VSP_008632;
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                         :soId=Q13231-3; Sequence=VSP_008633;
                                                                                IsoId=Q13231-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            back to normal
                                                                                                                                                                                                                                                                                                                                                                                                                        nsed;
                                                    Name=1;
```

CHT1_HUMAN STANDARD; PRT; 466 AA.
Q13231; Q9H3V8;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chitotriosidase 1 precursor (BC 3.2.1.14) (Chitinase 1).

RESULT 2
CHT1 HUMAN
ID CHT1 HI
DT 15-MAR
DT 15-MAR
DT 15-MAR
DT 15-MAR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EKRGYERFINILRLKUPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 YINNGATRDKIAMGVPFYGRAWSIEDRSKIKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 RIVCYVGIWSVYHKVDP-YIIEDIDPFKCTHLMYGFAKIDBYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                          Polysaccharide degradation, Hydrolase, Glycosidase, Chitin-binding,
Signal, Alternative splicing; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                            GO GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005617; P:response to bacteria; TAS.
GO; GO:0009617; P:response to bacteria; TAS.
GO; GO:0009617; P:response to peet/pathogen/parasite; TAS.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR001279; Glyco_hydro_18.
Pfam; PF01607; CBM 14; 1.
Prodom; PD000471; Glyco_hydro_18; 1.
SWART; SM00494; ChtBD2; 1.
SWART; SM00494; ChtBD2; 1.
PROSITE; PS01095; CHITINASE 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
ROSITE; PS01095; CHITINASE 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SL -> NG (in isoform 2).
/FIId=VSP 008631.
Missing (in isoform 2).
/FIId=VSP 008632.
Missing (in isoform 3).
/FIId=VSP 008633.
/FIId=VSP 008633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHITOTRIOSIDASE 1.
CHITIN-BINDING TYPE-2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.8%; Score 738; DB 1; 34.2%; Pred. No. 1.6e-33;
                                                                                                                   EMBL, U29615; AAC50246.1; -...
EMBL, U52662; AAG10644.1; -...
PDB; 1GUY; 31.JAN-02.
PDB; 1LG1; 18-SEP-02.
PDB; 1LG2; 18-SEP-02.
Genew; HGNC:1936; CHIT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 AA; 51681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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466
140
51
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417
140
26
307
386
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DISÜLFID
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Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alaxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richall P., Lewis S., Matsuo Y., Nikali C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikali C., King B., Kochiwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchbonni L., Mashima J., Marchaetts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hayashizaki Y., Mayashizaki Y., Marchional annotation of a full-length mouse cDNA collection.",
310 KGATKQRIQ-DQ--KVPYIFFDNQWYGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366
                                                                                                                     -----FSCNOG------RYPLIQTIRQELSLPYLPSGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Salivary gland;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer K. Mubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                         GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTFTTTPTTTPTTPTTPSPTTPTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE-Lung;
MEDLINE=21125893; PubMed=11085997;
Boot R.G., Blommaart B.F.C., Swart E., Ghauharali-van der Vlugt K.,
Bijl N., Moe C., Place A., Aerts J.M.F.G.;
"Identification of a novel acidic mammalian chitinase distinct from chitotriosidase.";
                                                                                                                                                                                                                                                                                                                                        CHIA_MOUSE STANDARD;
Q91XX3; Q99PH2; Q90803; Q9ULN1;
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase) (YNL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SEQUENCE OF 22-43, TISSUE SPECIFICITY, AND
                                                                                                                                                                      445 PSPTTPTTTPSPTTPSPTTPT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 276:6770-6778(2001).
                                                                                                                                                                                                                    395 PELEVP-KPGQPSEPEHGPSPGQDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                       ဗ
                                                                                                                       367
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75 KYTIQVFDPYQDDNHNSW-EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANP 133

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### EMBL; AK008633; BAB25795.1; -

### EMBL; AK008633; BAB25795.1; -

### EMBL; AK154571; AAH11134.1; ALT_INIT.

### EMBL; AR154571; AAH3164.1; -

### EMBL; AR154571; AR31644.1; -

### EMBL; AR154571; AR31644.1; -

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### MGD; MG1:1932052; Chia.

### EMBL; BR001253; Chia.

### Probon; PR001253; Chia.

### Probon; PR001279; Glyco_hydro_18.

### Probon; PR0014; Glyco_hydro_18.

### Probon; PR00494; Chia.

### SMART; SM00494; Chia.

### SMART; SM00494; Chia.

### ROSITE; PS01095; CHITINASE 18; 1.

### ROSITE; PS01095; CHITINASE 18; 1.

### Propredation degradation; Hydrolase; Glycosidase; Chitin-binding;

#### Propredation of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conte
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                            23.6%; Score 734.5; DB 1; Length 473; 36.3%; Pred. No. 2.5e-33; ive 72; Mismatches 148; Indels 57,
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473 CHITIN-BINDING TYPE-2.
140 BY SIMILARITY.
51 BY SIMILARITY.
53 BY SIMILARITY.
293 P -> A (IN REF. 1).
52003 MW; 333C874477476695 CRC64;
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                  cDNA sequences.
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473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                              306
                                                                                                                                                                                                                                                                                                              307 GFISGEEGVLSYIELCOLFOK---EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                            233 TETGS-NAYLAVVANYWANGAPAEKLIVGFPEYGHTFILRNPSDNGIGAPTSGDGPA
                                                                                                                                                                                                                                                                                                                                          292 GPYTRQAGFWAYYEICTFLRSGATEVW----DASQEVPYAYKANBWLGYDNIKSFSVKAQ
247 DETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPP
                                                                                                                                                                                                                                                                                                                                                                                                  364 PLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTT
                                                              134 TYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG--
                                                                                                                                            192 ----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
MEDIINE=22426071; PubMed=12537574;
HOSKINS R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila.", Insect Mol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heterochromatic sequences in a Drosophila whole-genome shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterayota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de la Vega H., Specht C.A., Liu Y., Robbins P.W., "Chitinases are a multi-gene family in Aedes, Anopheles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assembly.";
Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH11 DROME STANDARD; PRT; 508 AA. 109W512; 0.17420; 10.0CT-2003 (Rel. 42, Last sequence update) 10.0CT-2003 (Rel. 42, Last sequence update) 110.0CT-2003 (Rel. 42, Last annotation update) CHT1 OR CG17682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Canton-S;
MEDLINE=98324849; PubMed=9662472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 TPTPTTTPTTTP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 GCTAPDVPSEPVTTP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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74 64

57; Gaps

158; Conservative

Similarity

Local

Best Loca Matches

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LINAQLGSAXN-----LICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNN 16 LMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEY

13

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---EKRGYERFINILRLKNPELTTMISLGGWYEGS-EKYSDMAANPTYRQQFIQSVLDFLQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 ADLDNKFYERIVAYRKKGAKVT--VAIGGWNDSAGDKYSRLVRNPEARSRFIRNVLDFIE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 VIDAGYEVAELSHYFSWISYMAYDYHGQWDKKTGHVAPMYSHPEGT----ANFNANFSMN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 LFOKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDD 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |: |: |: |: |: || 3 || 3 || 428 KIRHHRMAVVRDIKGRIGPFAYHGDQWVSFDDVPMIRHKSEYIKAMGLGGAMIWALDLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 EYKFDGLDLDWEYP----GSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIŜSUE=Lung;
MEDLINE=20018184; PubMed=10548734;
Saito A., Ozaki K., Fujiwara T., Nakamura Y., Tanigami A.;
"Isolation and mapping of a human lung-specific gene, TSA1902,
encoding a novel chitinase family member.";
Gene 239:325-331(1999).
                                                                                          FlyBase; FBG0022703; Cht1.
InterPro; IRR00123; Glyco_hydro_18.
InterPro; IRR00123; Glyco_hydro_18As.
InterPro; IRR001579; Glyco_hydro_18As.
ProDom; PD000471; Glyco_hydro_18; 2.
ProDom; PD000471; Glyco_18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
AGT SITE 264 264 PROTON DONOR (BY SIMILARITY).
SEQÜENCE 508 AA; 57751 MW; 26CA23B02EFDEE97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 723; DB 1; Length 508; 39.8%; Pred. No. 1.1e-32; tive 71; Mismatches 121; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIA HUMAN STANDARD; PRT; 476 AA.
Q9BZP6; Q86UD8; Q9ULY3; Q9ULY4;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Acidic mammalian chitinase precursor (BC 3.2.1.14) (AMCase)
(TSA1902).
   send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
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TISSUE-Lung, and Stomach;
MEDLINE-21125893; PubMed=11085997;
                                                               EMBL; AF026500; AAB81858.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Bill W. Mee C., Place A., Aerce U. Mar. G.,

M. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification of a novel acidic mammalian chitimase distinct from R. Tidentification R. T. Faceberg B. Barcow R. H., Schaeler C.: Bark N. K.,

M. Michael R. F., Oschar H., Moore T., Max S.L., Marga J., Maich F.,

M. Michael R. F., Oschar H., Moore T., Max S.L., Marga J., Maich S.,

M. Michael R. F., Oschar H., Moore T., Max S.L., Marga J., Marga J., Maich S.,

M. Michael R. F., Oschar H., Moore T., Max S.L., Marga J., Marga J.,

M. Michael R. M., McGhan P.J., McGernan K.J., Marga J., Marga J., Malk J.,

M. Michael R. M., McGhan P.J., McGernan K.J., Marga J., Marga J.,

M. Michael R. M., McGhan P.J., McGernan K.J., Marga J., Marga J.,

M. Michael R. M., McGhan P.J., McGernan K.J., Marga J., Marga J.,

M. Michael R. M., McGhan J. McGernan K.J., Marga J., Marga J.,

M. Michael R. M., McGhan J., McGernan K.J., Marga J.,

M. Michael R. M., McGhan J., McGernan K.J., Marga J.,

M. Michael R. M., McGhan J., McGernan K.J., Marga J.,

M. Michael R. M., McGhan J., McGernan K.J., Marga J.,

M. Michael R. M., McGhan J.,

M. McGhan R. M., McGhan J., McGernan K.J., Marga J.,

M. Michael R. M., McGhan J.,

M. McGhan R. M., McGhan J., McGernan K.J., Marga J.,

McGharaga A., McGhan J.,

McGhan R. M., McGhan J., McGernan K.J., Marga J.,

McGharaga A. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

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McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., McGhan J.,

McGhan R. M., Mc

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388 GPKN----PLLNKVHNMINGDEKNSFECIL---GPSTTTPT-----
  MEDLINE=98324849; PubMed=9662472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             250 WKDNGAPAEKLIVGFPTYGHNFILSNPSNTGIGAPTSGAGPAGPYAKESGIWAYYEIC-T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 -EKRGYERFINILALKNPELITMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
                                                                                                                                                                                                                                                                                                                                              FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                                                                                                                                                  FDGLDFDWEYPGSR-GSPPQDKHLFTVLVQEMREAFEQEAKQINKPRLMVTAAVAAGISN 190
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                                                                                                                                                                                                                                                           RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                        IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-HCGP-KNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTPTTTPTTFS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
PROSITE; PS50940; CHIT BIND II; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Carbohydrate metabolism; Chitin degradation;
Polysaccharide degradation; Hydrolase; Glycosidase; Chitin-binding;
                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                 DB 1; Length 476;
                                                   BY SIMILARITY.
ACIDIC MAMMALIAN CHITINASE.
CHITIN-BINDING TYPE-2.
POLY-SER.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSING (in isoform 3).
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                           /FTId=VSP 008635.
I -> V (IN REF. 1).
V -> G (IN REF. 1).
92B27BAD2F7EB4CC CRC64;
                                                                                                                                       /FTId=VSP 008634.
Missing (in isoform 2)
                                                                                                                                                                                                                22.8%; Score 708.5; DB 1; 35.9%; Pred. No. 6.4e-32; ive 75; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIT CAEEL STANDARD; PRT; 617 AA. 011321, 1 01721, 1 0110V-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) CHT-1 OR 04766.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                 432 V
52271 MW;
                                           Signal, Alternative splicing.
SIGNAL 1 21
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140
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SEQUENCE OF 62-178
                                                                                                                                                                                                                          Similarity
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427
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DOMAIN
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DISULFID
DISULFID
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CONFLICT
SEQUENCE
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Best Local S
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                                                                                                                               VARSPLIC
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CHIT_CARE
ID TATE
ID TATE
AC 011174
DT 01-NOV
DT 01-NOV
DT 15-NAR
DB PTODAB
GN CAENOR
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OC BUARTY
OC BUARTY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 IDIDWEYPSG-----ATDMANYVALVKELKAACESEAGSTGKDRLLVTAAVAAGPATIDA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AYDIKELNKLFDWMNVMTYDYHGGWENPYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 KGMPKEKIIVGMPTYGRGWTLNNASAINPGTSGSPAKITQYVQ-EAGVGAYFEFCEMLAN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 G-YERPINILRIKNPELITMISLGGWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYKFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 LDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 GATR-YWDSQSQVPYLVQGNQWWSYDDEESFANKMAYVKREGYGGAFVWTLDFDDDFNAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PTTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKR
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 705.5; DB 1; Length 617;
Robbins P.W.;
in Aedes, Anopheles and
                                                                                                                                                            hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W -> C (IN REF. 2).

ITF -> TTS (IN REF. 2).

I -> L (IN REF. 2).

DDA1D2AAAC0E54DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mornep; C04F6.3; CE03923.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR001223; Glyco hydro_18.
InterPro; IPR001279; Glyco_hydro_18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan, PF01607; CBM 14, 2.

Pfam, PF00704, GlyCo_hydro_18, 1.

ProDom; PD000471; GlyCo_hydro_18, 1.
  la Vega H., Specht C.A., Liu Y.,
itinases are a multi-gene family
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30.2%;
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PIR; T15408; T15408.
PIR; T37249; T37249.
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167

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188 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
                                                                                                                                                                                              168 RREAQLIMRPRILLSAAVSADPHVIQKAYDVRLIGRLIDFINVLSYDLHGSWEKVTGHNS 227
                                                                                                                                                                                                                                                 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                                                                                                                                                                                                                                                                                                                    301 KGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASI 358
LLLWVGLV--LVLKHHNGAAH---KLVCYFANWA-FSRPGPASILPRDLDPFLCTHLVFA 57
                                                                                                                                                                                                                                                                                 228 PLFSLSDDPK-----SSAYTMNYWRKLGAPPEKLLMGFPTYGRTFRLLKASKNELGAEA
                                                                                                                         109 TMLSTFTNREKFIRSAIGLLRTHGFDGLDLFFLYPGLR-GSPRRDRWNFLFLLSELLLAF
                                                                                                                                                                                                                                                                                                                                                                                                             58 FASMIDSQIVAK-----DARD--BSIFYPEFNQLKERNEKLKTLLSIGGWNFGTSRFT
                                                                                                                                                                                                                                                                                                                                          282 VGPASPGKYTKQAGFLAYYEVCSFVQRAKKRW---IDHQY-VPYAYRGKEWVGYDDDISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 GLSTTVNSSRTCPESLAVTKOLTTOLGILPLGGBAVATETHGRSDNM-TVTPGGGLVAPT
                                  68 PAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERPNNLRLKNPELTTMISLGGWYEGSEKYS
                                                                                                       128 DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF
                                                                                                                                                                                                                                                                                                                                                                                           SCKLAFLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 GPSTTTPTPTTTPTTTP--TTPSPTTPTTTPSPTTTPSPTTTPSPTTTPSPTTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TPAPTTSTPSP-----TTTEHTSETP 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 RPTLSFGKLTVAPEGKTESPGEKAMTPVGHPSVTP 489
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Q28042;
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                                                                                       518
                SNSNGOLYPLISVIAKELGG------VIIPKKGGVTTAPTTVATTVTTGRPPMTSAVTT 458
                                                                                                                         SEQUENCE FROM N.A.

STRAIN=YORKBhire X Duroc X Hampshire; TISSUE=Oviduct;

MEDLINE=97107140; PubMed=849888;

Buhi W.C., Alvarez I.M., Choi I., Cleaver B.D., Simmen F.A.;

Buhi W.C., Alvarez I.M., Choi I., Cleaver B.D., Simmen F.A.;

"Molecular cloning and characterization of an estrogen-dependent
porcine oviductal secretory glycoprotein.";

Biol. Reprod. 55:1305-1314 (1996).

-I- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a role
in the fertilization process and/or early embryonic development.

-I- SUBCELLULAR LOCATION: Secretory granules.

-I- SINILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                     459 TTAATTTTTRAATTTTASNTNVCSGKSDGFYPNSNNCGLFVLCLSSKSYSMSCPSGLQYS
                                                                                                                                                          519 ASLKYCTTSTASGCSVTTTRAPTTTTKSAPT--VTTTTRAPTTT----TPAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
88-FBB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (POSP-E3).
                                                                                                                                                                                              552
                                                                                                                                                                                                                  --KCTKDGFFGVPSDCLKFIRC--VNG--ISYNFECPNGLSFHADTMMC 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31B78F49CA2363A2 CRC64;
                                                                                                                                                                                                                                                                                                                       527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58519 MW;
                                                    TTTPSPTTPSPTTPSPTT-
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
402
441
527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                               OVGP1 OR OGP.
                                                                                                                         450
                                                                                                                                                                                              504
                                                                                                                                                                                                                               265
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                   90‡
                                                    430
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                                                                                                                                                                                                                                                                                 RESULT 7
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                        BIO1. Reprod. 50:927-934(1994).
-!- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a rollin the fertilization process and/or early embryonic development.
-!- SUBCELDULAR LOCATION: Secretory granules.
-!- TISSUB SPECIFICITY: Oviduct.
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Fragment).
                                                                                                                                                                                                                                                                                                                    TISSUE-Oviduct;
MEDLINE=94257768; PubMed=8199272;
Sendal Y., Abe H., Kikuchi M., Sacoh T., Hoshi H.;
"Purification and molecular cloning of bovine oviduct-specific
537 AA
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 19-47.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D16639; BAA04065.1; -.
STANDARD;
                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein.";
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10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67

Matches 178; Conservative

8

Similarity

Local

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Gaps

59;

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                          Desouza M.M., Murray M.K.;
"An estrogen-dependent secretory protein, which shares identity with
                                                     chitinases, is expressed in a temporally and regionally specific manner in the sheep oviduct at the time of fertilization and embryo
                                                                                                                                               MEDLINE=96329120; PubMed=8726871;
                                                                               development.";
Endocrinology 136:2485-2496(1995)
                                                                                                                      SEQUENCE OF 10-539 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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  55 FASMSNNQ--IVPKDP-OD-----EKILYPEFNKLKERNRGLKTLLSIGGWNFGTVRFT 105
                                                                                                                                                                                                                                                                                                                                                       128 DWAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF 187
                                                                                                                                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                          188 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLYKRPDETDELHTYFNVNYTMHYYLINNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 PLFSLPGDPK-----SSAYAMNYWRQLGVPPEKLLMGLPTYGRTFHLLKASQNELRAQA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 VGPASPGKYTKQAGFLAYYEICCFVRRAKKRWINDQY--VPYAFKGKEWVGYDDAISFGY 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAFLKELGVSGVMVWSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 TPTP----TTTPTTPTTPSPTTPSPTTPSPTTP------TTTPSPTTPTTPSPT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPSPKFWFSTAVNSSRIGPEMPTWTRDLTTGLGILPPGGEAVATETHRKSETWTITPKGE 446
                                                                                                                                                                                                                                                                                                  68 FAKIDEYKYIIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTIMISLGGWYEGSEKYS 127
                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                            10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI---EDIDPFKCTHLMYG
                                                                                                                                                                                                                                                                                                                                                                                106 TMLSTFSNRERFVSSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWTFVFLLEELLQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                   165 KNEAQLIMRPRLILISAAVSGDPHVVQKAYBARLIGRLLDFISVLSYDLHGSWEKVIGHNS
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
Oviductin) (Estrogen-dependent oviduct protein) (Estrus-associated Oviducal glycoprotein) (Ocopi OR OGP)
                                                                                                                                                                                                                  69
                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                        22.1%; Score 685.5; DB 1; Length 537; 33:3%; Pred. No. 1.3e-30;
                                                                                                                                   OVIDUCT-SPECIFIC GLYCOPROTEIN N-LINKED (GLCNAC. . .) (POTENT; CFDCEE6F0212D791 CRC64;
                                                                                                                                                                                                                  95; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 IATPTRTPLSFGRHTAAPEGKTESPGEKPLTTVGHLAVSP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 TPTPT-TP-----TPAPTTSTPSP-----TTTEHTSETP 494
     InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.5.
Pfam; PF00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SWART; SW0636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; PALSE NEG Glycoprotein; Fertilization; Signal.
NUM TER 1 1 18
                                                                                                                      <1 18
19 537 OVJ
399 399 N-I
537 AA; 59617 MW; (
                                                                                                                                                                                                                 Matches 173; Conservative
 PIR; S57197; S57197.
                                                                                                                                                                                                      Similarity
                                                                                                                                               CARBOHYD
SEQUENCE
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                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                    CHAIN
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OGP_SHEEP
OGP_SHEEP
DD Q2854
DT 01-NO
DT 30-MA
DE Ovidu
DE Ovidu
DE Ovidu
DE Ovidu
OS OVIGPI
OC Bukar
OC Mamma
OC Mamma
OC NOCBI
RR 11] -
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 KMLSTFSNRERFVKSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWTFVFLLEELLQAF
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 539;
                                                                                                                                                                                          OVIDUCT-SPECIFIC GLYCOPROTEIN N-LINKED (GLCNAC. . .) (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                      13 M -> V (IN REF. 2).
122 K -> N (IN REF. 2).
282 A -> V (IN REF. 2).
375 A -> V (IN REF. 2).
444 R -> H (IN REF. 2).
59535 MW; F35000269987C193 CRC64;
                                                                                                                                                                                                                                                                                                                                                             22.0%; Score 685; DB 1; Le 33.8%; Pred. No. 1.4e-30; ive 90; Mismatches 185;
EMEL; U16719; AAC48471.1; -
EMEL; U19988; AAB01052.1; -
PIR; I46470; I46470
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
Frobom; P00004; Glyco hydro 18; 1.
Probom; P0000471; Glyco hydro 18; 1.
SWART; SW0636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; FALSE NEG Glycoprotein; Fertilization; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                173; Conservative
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Ovis aries (Sheep). Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.

SEQUENCE FROM N.A., AND SEQUENCE OF 22-39

NCBI_TaxID=9940;

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CHAIN
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                   EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
                                              PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                                                                                                                                                                                                         301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                                                                                                                                                                                                                                                                                                        KLAFLKELGVSGVMVWSLENDDPKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT 418
                                                                                                                                                                                                                                                                                                                                                                                                     TPTP----TTTPFTTPTTPSPTTPTTPSPTTP-----TTTPSPTTPTTPSPTTPTTPSPTTPSPT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                               390 TPSPXFWFSTAVNSSRIGPEMPTMTRDLTTGLGILPLGGEAVATETHRKSATMTTTPRGE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morrison B.W., Leder P.,
"neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.",
Oncogene 3:3417-3426 (1994)
-!- FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment (By
                                                                                                                                                                                                                                         282 AGPASPGKYTKQAGFLAYYEVCSFVQRAKKRWINDQY.-.VPYAFKGKEWVGYDDAISFGY
                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
(GP-39) (RRB39 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SUBCELLULAR LOCATION: Extracellular (By similarity).
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
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InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001529; Glyco_hydro_18A.
Pfam; PF00704; Glyco_hydro_18; 1.
Pr0Dom; PD000471; Glyco_hydro_18; 1.
SWART; SM00636; Glyco_18; 1.
PROSITE; P$01095; CHITINASE_18; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPTPT-TP----TPAPTTSTPSPTTTEHTS
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STRAIN-FVB/N; TISSUE-Breast;
MEDLINE-95060797; PubMed=7970700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X93035; CAA63603.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal.
SIGNAL
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Q61362;
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                   188
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MOUSE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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OGP MESAU SILL.

OGOPOST, OG0526;

01-NOV-1997 (Rel. 35, Last sequence update)

01-NOV-1999 (Rel. 38, Last annotation update)

15-UTL-1999 (Rel. 38, Last annotation update)

Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)

Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)

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                                                                                                             21.9%; Score 680; DB 1; Length 38 37.1%; Pred. No. 1.8e-30; tive 75; Mismatches 130; Indels
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CHITINASE-3 LIKE PROTEIN 1
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  381 CHITINASE-3 LIKE PROTEIN : 60 N-LINKED (GLCNAC. . .) (PC 43001 MW; EF6581E8184F0450 CRC64;
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"Allelic polymorphism in the hamster oviductin
variable number of mucin-like tandem repeats.";
Mol. Reprod. Dev. 42:388-396 (1995)
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TISSUE=Oviduct;
MEDLINE=96115007; PubMed=7492686;
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                                                                                                                                                                 141; Conservative
  22 3
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381 AA;
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SEQUENCE OF 14-67
TISSUE=Oviduct;
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                            CARBOHYD
SEQUENCE
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Best Local S:
Matches 141
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240

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282 MGPASPGKYIKQAGFLAYYEVCSFIQRAEKH--WIDHQYVPYAYKGKEWVGYDDAVSFSY 339
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                                                                               109 TWLSTLASREKFIGSVVSFLRTHGFDGLDLFFLYPGLR-GSPINDRWNFLFLIEELQFAF
                                                                                                                                                                                             241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                                                                                                                                                                                                 228 PLFSLPEDPK-----SSAFAMNYWRNLGAPADKLLMGFPAYGRTFHLLRESKNGLQAAS
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                                          DMAANPTYROOFIOSVLDFLOEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF
                                                                                                                                                              EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
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InterPro; IPR001223; Glyco.hydro.18.
InterPro; IPR001579; Glyco.hydro.18AS.
Pfam; PF00704; Glyco.hydro.18; I.
ProDom; PD000471; Glyco.hydro.18; 1.
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Q62010;
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SEQUENCE OF 22-39.

MEDLINE-94058981; PubMed=8240241;

Malette B., Bleau G.;

Malette B., Bleau G.;

"Biochemical characterization of hamster oviductin as a sulphated compellucida-binding glycoprotein.";

Eliochem. J. 295:437-445(1993).

"Eliochem. J. 295:437-445(1993).

"Eliochem. J. 295:437-445(1993).

"In the fertilization process and/or early embryonic development. Might act as a protective secretion influencing the first steps of the reproductive process necessary for the normal triggering of fertilization and early embryonic development.

"SUBCELIULAR LOCATION: Secretory granules.

"ITSUE SPECIFICITY: Oviduct.

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H -> I (IN REF. 4).
D -> G (IN REF. 2 AND 3).
R -> Q (IN REF. 2 AND 3).
F -> Y (IN REF. 2 AND 3).
Q -> L (IN REF. 2 AND 3).
MISSING (IN REF. 2 AND 3).
T -> I (IN REF. 2 AND 3).
Y, BB57E0E514EC1972 CRC64;
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Pred. No. 3.4e-30;
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R InterPro; IPR001223; Glyco_hydro_18.

R InterPro; IPR001259; Glyco_hydro_18AS.

ProDom; P000704; Glyco_hydro_18AS.

R ProDom; P0000471; Glyco_hydro_18; 1.

R ProDom; P0000471; Glyco_hydro_18; 1.

R PROSITE; P801095; CHITINASE_18; FALSE NEG.

Glycoprotein; Fertilization; Repeat; Signal.
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Similarity 33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning and characterization of a mouse oviduct-specific
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotetation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein).
Mus musculus (Mouse)

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ICR; TISSUS=Oviduct;
MEDLINE=96115001; Pubmed=7492680;
Sendai Y., Komiya H., Suzuki K., Onuma T., Kikuchi M., Hoshi H.,
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 WRKLGTPADKLIMGPPTYGRNFYLLKESKNGLQTASMGPASPGKYTKQAGFLAYYEVCSF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 VQRAKKH--WIDYQYVPYAFKGKEWLGYDDTISFSYKAMYVKREHFGGAMVWTLDMDDVR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TTTPTTPTTPTTPTTPSPTTP-----TTTPS--PTTPTTTPSPTTPSPTTTPSPTTPT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 FDGLDLFFLYPGLR-GSPPHDRWNFLFLIEELQPAFEREALLTQHPRLLLSAAVSGIPSI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 TEVLTTDTIKILPPGGEAMTTEVHRRYENMTTVPSDGSVTPGGTASPRKHAVTPENNTMA 473
                                                                                                                                                                                                                                                                                                                                                                                                              WEKRGYER FINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                                                                                                                                                                                                                                                                                                                                                     23 KLVCYFTUWA-HSRPGPASIMPHDLDPPLCTHLLFAFASMSNNQI---VAKNLQDENVL- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 IHTSYDALLLGRRLDFINVLSYDLHGSWEXFTGHNSPLFSLPEDSK-----SSAYAMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDGLDLDWEYPGSRLGNPK1DKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDK
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                                                                                                                                                                                                                                                                                                                              34 RIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNS
                                                                                                                                                                                                                                                                                         82; Gaps
                                                                             OVIDUCT-SPECIFIC GLYCOPROTEIN.

21 X 7 AA TANDEM REPEATS OF S-K-T-T-
[TAP] -G-[IV].
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGP_HUMAN STANDARD; PRT; 678 AA.
012803; Q15804; Q15804;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last annotation update)
00'siduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Mucin 9).
00'GP1 OR OGP OR MUC9.
                                                                                                                                                                                                                                               21.9%; Score 680; DB 1; Length 721; 33.7%; Pred. No. 3.6e-30; cive 79; Mismatches 184; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Oviduct;
MEDLINE=99119256; PubMed=7819450;
Arias E.B., Verhage H.G., Jaffe R.C.;
"Complementary deoxyribonucleic acid cloning and molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-HCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPTP----
                                                                                                                                                                                                       37246C8F01665652 CRC64;
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                                     Repeat; Signal.
                       FALSE NEG
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18;
Glycoprotein; Fertilization; Rep
                                                                                                                                          402 N-
442 N-
469 N-
78807 MW;
                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.7%;
...nes 175; Conservative
                                                                               721
632
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                                                                                                                                                               442 4
469 4
721 AA;
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                                                                                 22
486
                                                                                                                                            402
                                                                                                                                                               CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal, Polymorphism.
BY SIMILARITY.
OVIDUCT-SPECIFIC GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192; Indels
characterization of an estrogen-dependent human oviductal
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N-LINKED (GLCNAC. .) (POTI
N-LINKED (GLCNAC. .) (POTI
N-LINKED (GLCNAC. .) (POTI
FITIGA'VR 016109.
M -> T (IN REF. 2).
Y -> H (IN REF. 2).
Y -> H (IN REF. 2).
                                                                                                                  Jaffe R.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 33.1%; Pred. No. 1.5e-29;
es 176; Conservative 91; Mismatches 192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603578; ...
GO, GO:0007565; P:pregnancy; TAS.
InterPro; IPR001223; Glyco_hydro_18.
InterPro: IPR001579; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 1.
Pr0Dom; PD000471; Glyco_hydro_18; 1.
PRODTE; PS01095; CHITIMASE 18; FALSE NEG.
Glycoprotein; Pertilization; Signal; Polymory SIGNAL
                                                                                        SEQUENCE FROM N.A., AND VARIANT GLN-676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, U09550; AAA66946.1; ...
1, U580010; AAB04126.1; ...
1, U580011; AAB04126.1; ...
1, U58002; AAB04126.1; JOINED.
1, U58003; AAB04126.1; JOINED.
1, U58004; AAB04126.1; JOINED.
1, U58006; AAB04126.1; JOINED.
1, U58009; AAB04126.1; JOINED.
1, U58009; AAB04126.1; JOINED.
1, U58009; AAB04126.1; JOINED.
1, U58009; AAB04126.1; JOINED.
1, U58009; AAB04126.1; JOINED.
1, AL390195; CAC36039.1; -1
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· 75421 MW;
                    lycoprotein.";
iol. Reprod. 51:685-694(1994)
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678
4402
580
596
678
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678 AA;
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EMBL; M80927; AAA16074.1; -...
EMBL; Y08374; CAA69661.1; -...
EMBL; Y08375; CAA69661.1; JOINED.
EMBL; Y08376; CAA69661.1; JOINED.
EMBL; Y08379; CAA69661.1; JOINED.
EMBL; Y08379; CAA69661.1; JOINED.
PIR; A49562.
PDB; ILA7; 10.2ARF-02.
Genew; HGNC.1932; CH1311.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; 3D-structure
mononuclear cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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OGP_PAPAN
ID OGP_PAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                     RKEALLTWRPRLLLSAAVSGVPHIVQTSYDVRFLGRLLDFINVLSYDLHGSWBRFTGHNS 227
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                                                                                                                                                               301 KGMSPPGFISGEEGVLSYIELCQLF--QKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASI 358
                                                                                                                                                                                                                                                                       282 IGPASPGKYTKQEGFLAYFEICSFVWGAKKHW----IDYQYVPYANKGKEWVGYDNAISF 337
                                                                                                                                                                                                                                 390 İSLPQFWLSSAVNSSSTDPERLAVITAMİTDSKILPPGGEAGVİEIHGKCENMİLIPRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Cartilage;
MEDIATE=9464689; PubMed=8245017;
MEDIATE=9464689; PubMed=8245017;
Hakala B.E., White C., Recklies A.D.;
"Human cartilage gp-39, a major secretory product of articular chondrocytes and synovial cells, is a mammalian member of a chitinase procein family.";
T. Biol. Chem. 268:25803-25810(1993).
                                                                                                                                   PLFSLPEDPK-----SSAYAMNYWRKLGAPSEKLIMGIPTYGRTFRLLKASKNGLQARA
                   SCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KNPLLNKVHNMINGDEKNSFECILGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=9032898); PubMed=2375755;
MEDLINE=9032898); PubMed=2375755;
Nyitxos P., Golds E.E.;
"Human synovial cells secrete a 39 kDa protein similar to a bovine mammary protein expressed during the non-lactating period.";
Biochem. J. 269:265-268 (1990).
-!- FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment.
-!- SUBCELINIAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Present in articular chondrocytes, synovial cells as well as in liver. Undetectable in muscle tissues, lung,
  128 DMAANPTYRQOFIQSVLDFLQBYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF
                                                       EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNA
                                                                                                            PLYKR PDETDELHTY FNVNY TMHYYLNNGATRDKLVMGV PFYGRAWS I EDRSKLKLGDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rehli M., Krause S.W., Andressen R.; Molecular characterization of the gene for human cartilage gp-39 (CHI3LI), a member of the chitinase protein family and marker for late stages of macrophage differentiation."; Genomics 43:221-225(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Last sequence update)
10-027-2003 (Rel. 42, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
39) (39 kDa synovial protein) (YKL-40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=97386591; PubMed=9244440;
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P36222; P30923;
O1-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CTHIIYSFANI-----SNDHIDTWEWNDVTLYGMLNTARNENDKTLSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 ALVRELKDAF----EP--HGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 WENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTHIMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRG---YERFNNIRLKNPELTTMISLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 601525; ...

GO; GO:0005578; C:extracellular matrix; TAS.

GO; GO:0005519; C:extracellular space; TAS.

GO; GO:000510; F:extracellular space; TAS.

InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001579; Glyco_hydro_18.

InterPro; IPR001579; Glyco_hydro_18.

Probom; PD000471; Glyco_hydro_18; 1.

SMART; SM00636; Glyco_hydro_18; 1.

PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
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      pancreas, mononuclear cells, or fibroblasts.
PTM: Glycosylated.
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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N-LINKED (GLCNAC. . .) (POT
76ADD8298EEEC2D1 CRC64;
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or fibroblasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                         Verhage H.G., Fazleabas A.T., Mavrogianis P.A., O'Day-Bowman M.B., Donnelly K.M., Arias B.B., Jaffe R.C.; "The baboon oviduct: characteristics of an oestradiol-dependent
                                                                      Papio anubis (Olive baboon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Papio.
        01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last amotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.1%; Score 654.5; DB 1; Length 623; 30.7%; Pred. No. 7.6e-29; ive 87; Mismatches 200; Indels 121;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                 MEDLINE-91367180; PubMed-1716345;
Donnelly K.M., Fazleabas A.T., Verhage H.G., Mavrogianis P.A.,
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InterPro; IPR001223; Glyco hydro 18.

InterPro; IPR001223; Glyco hydro 18.

Ffam; P00704; Glyco hydro 18; 1.

ProDom; P0000471; Glyco hydro 18; 1.

SMART; SM00636; Glyco 18; 1.

PROSITE; PS01095; CHITINASE 18; FALSE NEG.
                                                                                                                                                                                                                                              PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                             oviduct-specific glycoprotein.";
Hum. Reprod. Update 3:541-552(1997).
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                                                                                                                                                                 MEDLINE=98244335; PubMed=9584944;
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                                                                                                                     NCBI_TaxID=9555;
                                                                                                                                                                                                                                                          TISSUE=Oviduct
                                                                 OVGP1 OR OGP.
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SEQUENCE
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109 TMLSTPANREKFIASVISLLRTHDFDGLDLFFLYPGLR-GSPWHDRWTFLFLIEELLFAF 167
                                                                                                     188 EPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMWMTYDYHGGWENFYGHNA 240
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Search completed: March 22, 2004, 06:53:04 Job time : 23.2868 secs

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Mon Mar 22 11:57:32 2004
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Q9u6r7 dermatophag
044079 anopheles g
0818h5 araneus ven
017412 aedes aegyp
09w2z3 drosophila
09gqc4 bombyx mori
08mp6 tenebrio mo
08wr52 bombyx mori
01593 penaeus jap
09gr93 bombyx mori
09gy05 bombyx mori
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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Maximum DB seq length: 200000000
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QBMTKO	Q90W34	Q9GV44	017411	023737	026042	Q9Y0D4	P91731	Q803B7	Q86LZ2	Q7ZV48	Q13231	Q99PH2	O9JINI	090803	Q8AV87	Q9H3V8	Q95M17	Q8MS85	Q960M0	P91773	Q8WS95	Q9W092	O9BZP6	Q8MY79	Q9VZV2	Q9W2M6	Q99J84	Q8BKL8	ALIGNMENTS
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	AA.	.ed)	annotation update			Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,	Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea Dyroglyphidae: Dermatophagoides				Allergen	ı	to the EMBL/GenBank/DDBJ databases.				no br	; IEA.										0 0000000000000000000000000000000000000		DB 5;	Fred. No. 2.9e-18b; Mismatches 0;
	555	פטעפונ	otatio		mite	iceral	ta; P			McCall	98 kDa		Bank/1		:	Ά.	, act:	olism	IEA.	¥.		Š.							44144	3107;	red. No. 2. Mismatches
	PRT;	Created)			Dermatophagoides farinae (House-dust mite).	la; chel	Astigma				"Cloning and Characterization of a 9		MBL/Ger	;	C:extracellular; IEA.	F:chitin binding; IEA.	F:hydrolase activity, actin	se metak	P:chitin metabolism; IEA.	oind_Per	/dro_18.	InterPro, IPR001579; Glyco_hydro_18AS.	-i -i	.1 ,81-		,	18; 1.			Score 3107;	Pred. O; Mism
		13,	25,		e (Hor	hropod	rmes;	, ,		Stedma	zatio	 	the 1	2.1;	cellu.	n bin	lase a	hydrai	n met	itin_)	yco_h	yco_h	dro 18	_nyar(10	CHITINASE_18;	55. Mar.	20	100.0%;	*
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	PRELIN	(Treme	(Trem	lergei	ides	letazos	Sarce	954,	Z N	Hunter	Chare	ides	UG-19	72; A					30; P	R0025	R0012	R0015	4; GL)	(T/ #0	2.6	SMOUGAB; GLYCO	1095;	1 4 4	222 AA		Conservative
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1 1	Q9UGR7 O9UGR7;	01-MAY-2000	01-OCT-2003	98kDa HDM allergen.	Dermat	Eukary	Acariformes, Sarcoptiformes, Ast Pyroglyphidae: Dermatophagoides	NCBI_TaxID=6954;	LIJ SEOTENCE FROM N.A.	Weber	"Cloni	Dermatophagoides	Submitted (AUG-1999)		89			8 8	8	InterP	InterP	InterP	Pram; Pro0704; Glyco hydro 18; 1.	Frond	SMAKI;	SMAKI;	PROSITE; PS01095;	orycosidae, mydioidae.	S S S S S S S S S S S S S S S S S S S	Query Match	best Local Similarity Matches 555; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Han J.H., Kim S.R., Sohn H.D., Jin B.R.;
"Molecular cloning of a cDNA encoding the chitinase from the spider,
                                                                                                                                               DB 5; Length 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Ara
Araneomorphae, Entelegynae, Araneoidea, Araneidae, Araneus.
NCBI_TaxID=182803;
                                                                                                                                             32.5%; Score 1008.5; DB 5; Length 38.4%; Pred. No. 4e-55; vative 93; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Araneus ventricosus.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY120879; AAN39100.1; -
                                                                                                               525 AA; 57211 MW; 3234360EEFF36165 CRC64;
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Pfam; PF01607; CBM 14; 1.
Pfam; PF00704; Glyco hydro 18; 1.
ProDom; P0000471; Glyco hydro 18; 1.
SWART; SW00494; ChtBD2; 1.
SWART; SW00636; Glyco 18; 1.
PR0SITE; PS01095; CHTINASE 18; 1.
Glycosidase; Hydrolase.
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                                                                                                                                                                                211; Conservative
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"Lualou Chem. 272:28895-28900(1997).

"B Biol. Chem. 272:28895-28900(1997).

"B RMBL; AF008575; AAB87764.1; -.

"R GO; GO:0008057; C:extracellular; IEA.

"R GO; GO:0008061; F:chitin binding; IEA.

"GO; GO:0008061; F:chitin binding; IEA.

"GO; GO:0008075; P:carbohydrate metabolism; IEA.

"R GO; GO:0008075; P:carbohydrate metabolism; IEA.

"R GO; GO:0008075; P:chitin metabolism; IEA.

"R GO; GO:0008075; P:chitin metabolism; IEA.

"R GO; GO:0008037; Chitin bind PerA.

"R InterPro; IPR001223; Glyco_hydro_l8.

"R InterPro; IPR001579; Glyco_hydro_l8AS.
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                                   MKTIYAILSIMACIGLMAASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                                                                 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFINILRLKNPELTTMISLGGWY
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                                                                                                                                             EGSEKYSDMAANPTYROOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae (African malaria mosquito).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
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.057 PTRPPTS------TTPETTRRPSTTTSTRRTTMTTTT--TTTRRPTTTTRRRTSAR 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 DRLVIK------PHDSWADIDNRFYERVVEYKKKGKKVT--VAIGGWNDSAGDKYSRL 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 YKYTIQVFDPYQDDNHNSW---EKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPK----IDKQNYLALVRELKD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              937 AGESTRARGFLSYYEICANIRNKKWTVARDRKGRMGPYAYKGDQWVSFDDQYMIRHKSEY 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECIL--GPSTTTPT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IKRDHNDYSKNPM-----RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650 INKETSNODENAIESDVDYKVVCYFTNWAWYROGNGKYLPEDIDADLCTHIVYGFAVLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 PSPTTTEHTSETPKY-----TTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                on glycosyl bonds; IEA
                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 1635;
                                                                                                                                                                                           PROSITE; PRO1095; CHITINASE 18; 3.
Hydrolase; Glycosidase; Chitin degradation; Glycoprotein;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                            95; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                1635 AA; 185993 MW; EA116F83AAC129FA CRC64;
                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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N-LINKED (GLCNAC. ..)
GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0008043; F:chitin binding; IEA.
GO; GO:000843; F:chitin binding; IEA.
GO; GO:000575; P:carbohydrate metabolism; IEA.
GO; GO:000575; P:chitin catabolism; IEA.
InterPro; IPR00123; Glyco hydro 18.
InterPro; IPR00123; Glyco hydro 18.
InterPro; IPR00129; Glyco hydro 18.
Pfam; PF01704; Glyco hydro 18; 3.
Pfam; PF00104; Glyco hydro 18; 3.
ProDom; PP000491; Glyco hydro 18; 3.
SMART; SW00494; CheBD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 869; DB 5; 34.3%; Pred. No. 8.3e-46;
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                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
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322
463
749
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1338
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VARPTPDPK 403
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                                                                                                                                                                                                                                                                                    69 AKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSD
                                                                                                                                                                                                                                                                                                                                                 MAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFE
                                                                                                                                                                                                                                                                                                                                                                                                                PHGYLLTAAVSPGKDKIDRAYDIKELNRCFDWRNVMTYDYHGGWENFYGHNAPLYKRPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 -PESDKILNVDYAINYWIKNGTPKNKVILGMGTYGRSFTLANAANNGLGAATTGPGSAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 PHGLLLSAAVSAGKNTIDTAYDIPGVAKYLDFINVMAYDLHGSWEKTAGHNAPLYERPGE
                                                                                                                                                                                                                        12 ACIGLM -- NASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGF
                                                                                                                                                                                                                                                    ACLLILLUAVAVSAQSRDRNQKKYKVVCYLGSWANYRGGEGKFLIEHIDPFLCTHVIYGF
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotā; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBI_TaxID=7159;
                                                                                                                                                                                         26;
                                                                                                                                                        30.3%; Score 942; DB 5; Length 431; 43.6%; Pred. No. 4.6e-51; ive 78; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robbins P.W.;
in Aedes, Anopheles
                                                                                                                           47238 MW; 929439397B9BC923 CRC64;
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1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable chitinase 2 (EC 3.2.1.14).
GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001233; Glyco_hydro_18.
InterPro; IRBO01579; Glyco_hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
PRODOM; PD0000471; Glyco_hydro_18; 1.
PROSITE; SMO0565; Glyco_18; 1.
PROSITE; PS01095; CHITINAS 18; 1.
SEQUENCE 431 AA; 47238 MW; 929439397B9BC923 CR
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MEDLINE=98324849; PubMed=9662472;
de la Vega H., Specht C.A., Liu Y.,
"Chitinases are a multi-gene family
Drosophila.";
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PIR; T14075; T14075.
                                                                                                                                                                         Local Similarity 43.6
les 185; Conservative
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01-MAR-2001
01-OCT-2003
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Query Match
                        Best Local
Matches 20
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                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                            Last sequence update)
Last annotation update)
  PRT; 4498 AA.
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InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
Pfam; PF01607; CBM 14; 1.
Pfam; PF01607; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
                                                      Created)
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SMART; SW00636; Glyco_18; 1.
SMOSITE; PS01095; CHITINASE_18; 1.
Glycosidase; Hydrolase.
SEQUENCE 4498 AA; 493096 MW; AI
                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                   01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley
                                                                                                                                     CG2989 protein.
                                                                                                                                                              CG2989
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY 366
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Mititain x., Sudgaski r., Shimada T., Kobayashi M., Gustafsson J.A.;

Mititain x., Sudgaski r., Shimada T., Kobayashi M., Gustafsson J.A.;

Mititain x., Sudgaski r., Shimada T., Kobayashi M., Gustafsson J.A.;

The Chitinase Gene of the Silkworm, Bombyx mori, Contains a Novel Tc-
like Transposable Element.";

II. J. Biol. Chem. 275:37725-37732(2000).

MBL, AF273695; AAG37105.1; -.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

R GO; GO:0006001; P:chitin metabolism; IEA.

R GO; GO:0006030; P:chitin metabolism; IEA.

R GO; GO:0006057; Chitin metabolism; IEA.

R InterPro; IPR002557; Chitin_bind_PerA.
                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 ISETPKYTIYVDGHLIKCYKEGDIPHPINIHKYLVCEFVNG----GWWVHIMPCPPG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 -------GSDFKCEEBGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566
                                                                                                                                                                                                                                                                                                                                                                    129 AIGGWNEASSRFSPLVASNERRQQFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                               NYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 AYRRNQWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 NGDEKNSFECILGPSTTTPTTTTTTTTTTTT------TPSPTT----PTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 ----KEAMVEALGIGINEVAKPSGPOKPSRSRSNDNASNRNNRLNGKTEAPLSSRRPSATR
                                                                                                                                                                                                                                                       YHGGWENFYGHNAPLYKRPDETDELHTY - - - FNVNYTMHYYLNNGATRDKLVMGVPFYGR
                                                                                                             2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID
                                                                                                                                                                                                                       PFKCTHIMY---GFAKIDBYKYTIQVFDPYQDDNHNSWEKRGYERFNNIRLKNPELTIMI
                                                      Indels 119;
Length 4498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 RPAVSSTQAPP--PSTTFKLITEAEGSSLYIGGRASTTPPPPPTTPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
  27.5%; Score 854.5; DB 5;
33.8%; Pred. No. 2.2e-44;
tive 88; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                      88;
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16,
25,
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                                                         Conservative
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2448 PAPVGGTDVTEGAYKVVCYFTNW--AWYRQGD------GKYLPQDIDASLCTHINYGFA 2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1979 -----FDNKFYEKVTAFKAKG--IKVLIAIGGWNDSAGDKYSRLVNNPSSRRRFIAHVVD 2031
"A Novel putative insect Chitinase with multiple catalytic domains:

"Universal regulation during metamorphosis.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AJ487081; CAD3140.4; ...

BMGO; GO:0008061; Fichitin binding; IEA.

GO; GO:0008061; Fichitin binding; IEA.

GO; GO:0006520; P: Minton acid metabolism; IEA.

GO; GO:0005520; P: Minton acid metabolism; IEA.

GO; GO:0005520; P: Minton acid metabolism; IEA.

GO; GO:0005530; P: P: Chitin bind PerA.

BR GO; GO:0005530; P: Chitin bind PerA.

INTERPRO; IPR001223; Glyco_hydro_18.

INTERPRO; IPR001223; Glyco_hydro_18.

PEAM; PRO1004; Glyco_hydro_18; S.

PEAM; PRO1004; CHEDS.

PEAM; PRO1004; CHEDS.

PEAM; PRO1004; Glyco_hydro_18; S.

BRART; SM000494; CHEDS.

PROSITE; PS001055; GHYDRARĀŠE_SRA_THR; 1.

SURARI; SM00165; GHYDRARĀŠE_SRA_THR; 1.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNHNSWEKRGYERFNNLRLKNPELTIMISLGGWYEGS-EKYSDMAANPTYROOFIOSVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLOEYKFDGLDLDWEYP-----GSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMHYYLINNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCOLFOKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPTPKPSTPPYEPQKPSTQKPSYGTTESPEPVMPPDSVPCRGRLFVADEKNCNQYYLCNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2388 GELQLQVCPNGLFWNRDHCDWPENTECHPDGTTTAAPSTTTQTLEVEVEVEVEVTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYL------VCEFVNGGWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 NP---MRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKOKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPT--PTTTPT-TPTTFT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN 21 2838 CHITINASE.
SEQUENCE 2838 AA; 321407 MW; 608B3F2A8E98B9B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 DICTHLIXSFIGVTEXSSEVLIIDPELD-----UDKSGFRNFTSLRSKHPDVKFMVAVGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGHNAPLYKRPDETDELHTYFNVNYTWHYYLNNGATRDKLVMGVPFYGRAMSIED----- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 ADVHSPLYKRPHD-QWAYEKLNVNDGINIWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 GLGTYINKEAGGGDPAPYTNATGF-----WAYYEICTEVDADGSGWTKKWDEFGKCPY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AYKGTOWVGYEDPRSVEIKOMWIKEKGYLGAMTWAIDMDDPKGLCGEENPLIKLLH---- 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDEKNSFECILGPSTT---TPTPTTTPTTTPTTTPSPTTTPSPTTTPSPTTTPSPTTP 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KHMSTYTVPPARTGHATPTPEW--ARPPSTPSDPSEGDPI----PTTTTTVKPTTT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITPSPITPIPITPIPAPITSTPSPITTEHISETPKYTIYVDGHLIKCYKEGD-IPHPIN 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 RTTARPT--TTTTKVPHGTTEEDFDINVRPEVEEPPTENBVDNADV-CNSEDDYVPDKKE 502
                                                                                                                                                                                                                                                                                                                                                                                                                                      167 YFVQELKRAFIRADRGWELTAAVPLANFRLMEGYHVPELCOELDAIHVMSYDLRGNWAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVRELKDAF -- EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
                                                                                                                                                                                                                                                                                                                                                                                                     1 MKTIYAILSIMA-CIGLANASIKRDHNDYSKAPMRIVCYVGTWSVYHK-VDPYTIEDIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     64;
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tenebrio.
                                                                                                                                                                                                                                                                                               Length 544;
                                                                                                                                                                                                                                                                                               27.3%; Score 847; DB 5; Length 54
36.5%; Pred. No. 5.2e-45;
ive 78; Mismatches 218; Indels
  InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF01607; CBM 14; 1.
Prom; PF01607; CBM 14; 1.
ProDom; PF000471; Glyco_hydro_18; 1.
SMART; SM00494; ChtBD2; 1.
SMART; SM00636; Glyco_18; 1.
SMART; SM00636; Glyco_18; 1.
Glycosidase, Hydrolase.
Stycosidase, Hydrolase.
SEQUENCE 544 AA; 61069 MW; 89872DFC1DA23753 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 CSKYWRĆ--VNGEGVQ--FSCOPGTIF 525
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Royer V., Fraichard S., Bouhin H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Create 01-OCT-2002 (TrEMBLrel. 22, Last s 01-OCT-2003 (TrEMBLrel. 25, Last a Chitinase precursor (EC 3.2.1.14). CHITS.
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Best Local Similarity
Matches 207; Conserv
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339 AYKGTQWYGYEDPRSVEIKANWIKEKGYLGAMTWAIDMDDFKGLCGEENPLIKLHKHMS 398
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                                                                                                                                                                                                     445 TRTTARPTT------TTTKVPHGTTEEDFDINVRPEVEELPT-ENEVDNADV-CNSE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 WEKRGYERFINILKINPELTTMISLGGWYEGSEKYSDMAANPTYROOFIQSVLDFLQEYK 151
343 GYNDKIWYGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KCAYDRFTALKQQNANLKALLAVGGWNGGSPKYSKWAADPALRNRFITSSIELLKKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 FDGLDMDWEYPTQRGGSPD-DYDNFAILMAELKQALQPEGMLLTAAVSAGKATIDPAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 KELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRP-DETDELHTYFNVNYTMHYYLNNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD--DNHNS
                                                                                                                           ------TYTVPPARTGHTTPTPEWARP-PSTPSDPSEGDPIPTTTTVKPTT
                                                                                                                                                                       PTTTPSPTTPTTTTTPTPAPTTSTPSPTTTE------HTSETPKYTTYVDGHLIKCYKE
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Watanabe T., Kono M., Aida K., Nagasawa H.;

"Purification and molecular cloning of a chitinase expressed in the hepartpancreas of the penaeid prawn Penaeus japonicus.";

Blochim. Blophys. Acta 0.0-0(1997).

EMBL; AB008027; BAA22854.1; -.

ESSP; P07254; ICTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Bumalacostraca, Bucarida, Decapoda, Dendrobranchiata, Penaeoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO GO:0005576 C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000578; F:chitin binding; IEA.
GO; GO:000578; F:chitin binding; IEA.
GO; GO:000578; P:carbohydrate metabolism; IEA.
GO; GO:000570; P:chitin metabolism; IEA.
InterPro; IPR001223; Gilyco hydro 18.
InterPro; IPR00123; Gilyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
InterPro; IPR00167; CBM 14; 1.
InterPro; IPR00167; Glyco hydro 18; 1.
InterPro; IPR00167; Glyco hydro 18; 1.
INTERPRO; IPR0018; Glyco hydro 18; 1.
SWART; SM00434; Glyco hydro 18; 1.
SWART; SM00636; Glyco lig; 1.
RROSITE; PS01959; CHITINASE 18; 1.
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Last sequence update)
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                                                                                                                                                                                                                                                         GD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
                                                                                                                                                                                                                                                                               494 DDYVPDKKECSKYWRC--VNGEGVQ--FSCQPGTIF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score 837.5; DB 5; 34.8%; Pred. No. 1.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                        467 AA
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penaeus japonicus (Kuruma prawn)
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penaeidae; Marsupenaeus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLGTYINKEAGGGDPAPYINATGF-----WAYYEICTEVDADGSGWIKKWDEFGKCPY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLCTHILYSFIGVTEKSSEVLIIDPELD----VDKSGFRNFTSLRSKHPDVKFWVAVGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WYEGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKONYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 YFVQELKRAFIRAGRGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGF 226
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                                                                                                                                                                                                                                                             Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Kinshu x Showa; TISSUB=Integument;
Abdel-Banat B.M.A., Koga D.;
"Alternative mRNA splicing generates heterogeneity within Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene for chitinase.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF45519; AAL51080.1; --
EMBL; AF45519; AAL51080.1; --
EMBL; AF45519; AAL51080.1; --
GO; GO:0008576; Cextracellular; IEA.
GO; GO:000861; F:chitin binding; IEA.
GO; GO:0008843; F:endochitinase activity; IEA.
GO; GO:0008975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR0012557; Chitin metabolism; IEA.
InterPro; IPR0012257; Chitin bind PerA.
InterPro; IPR001229; Glyco_Bydro_I8.
InterPro; GO; GO:0008975; Chitin bind PerA.
InterPro; GO; GO:0008975; Chitin bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO; GO:0008975; Chitin Bind PerA.
InterPro; GO:0008975; Chitin Bind PerA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43FC717B3F6917D0 CRC64;
                                                                                                                                                                               Last sequence update)
Last annotation update)
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CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan, PFO1607; CBM 14; 1.
Pfam; PFO1607; CBM 14; 1.
Probom; PPO0704; Glyco hydro 18; 1.
SWART; SWO0494; ChrBD2; 1.
SWART; SWO0636; Glyco 18; 1.
SRART; SMO0636; Glyco 18; 1.
Signal; Hydrolase; Glycosidase.
Signal; Hydrolase; Glycosidase.
                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Chitinase precursor (EC 3.2.1.14).
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             2499 VLDGSTMTLKPHDSW 2513
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Matches 207; Conservative
                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                               Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7091;
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                                                                                                                QBWR52
QBWR52;
                                                                         RESULT 8
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226 ADVHSPLYKRPHD-QMAYEKLNVNDGLNLWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 284
                                                                                                                                                                                                                                                                                                            291 -----RSKLKGGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY 342
                                                                                                                                                                                                                                                                                                                                                                                          343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Kinshu X Showa hybrid; TISSUS=Integument;

X MEDLINES-1124800; PubNed=1122960;

RA Abdel-Banat B.M.A.; Koga D.;

RA Abdel-Banat B.M.A.; Koga D.;

RI "A genomic clone for a chitinase gene from the silkworm, Bombyx mori:

RT structural organization identifies functional motifs.";

Insect Biochem. Mol. Biol. 31:497-508(2001).

BR GO; GO:0005576; C:extracellular; IEA.

BR GO; GO:0008061; F:chitin binding; IEA.

BR GO; GO:0008061; F:chitin binding; IEA.

BR GO; GO:000575; P:chitin metabolism; IEA.

BR GO; GO:000575; P:cathonydrate metabolism; IEA.

BR GO; GO:000575; P:cathonydrate metabolism; IEA.

BR GO; GO:000575; Citin metabolism; IEA.

BR GO; GO:000575; Citin metabolism; IEA.

BR InterPro; IPR001257; Glyco_hydro_18AS.

BR InterPro; IPR001579; Glyco_hydro_18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bombyx mori (Silk moth).
Bukaryct; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                              338 AYKGTQWVGYEDPRSVEIKANWIKEKGYLGAMTWAIDMDDFKGLCGEENPLIKLLHRHMS
59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG
                     51 DLCTHLIXSFIGVTEKSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDVKFMVAVGG
                                                                                             106 WAEGGSKYSHWVAQKSTRMSFIRSVVDFLXKYDFDGLDLDWEYPGAADRGGSFSDKDKFL
                                                                                                                                                                               398 -----THIVPPARIGHTTPTPBWARP-PSTPSDPSEGDPIPTTTTTVKPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 TRTTARPTT-----TTTKVPHGTTEEDFDINVRPEVEELPT-ENEVDNADV-CNSE
                                                                           119 WYEGSEKYSDMAANPTYROOFIOSVLDFLOEYKFDGLDLDWEYPGSR-LGNPKIDKONYL
                                                                                                                                                       178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
                                                                                                                                                                                                                                   236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----
                                                                                                                                                                                                                                                                                                                                                  285 GLGTYINKEAGGGDPAPYTNATGF-----WAYYEICTEVDADGSGWTKKWDEFGKCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 PTTTPSPTTPTPTTPTPAPTTSTPSPTTTE-----HTSETPKYTTVVDGHLIKCYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 GDEKNSFECILGPSTTTPTFTTPTTPTTPTTPSPTTPTT----TPSPTTPTTTPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chitinase precursor (BC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 GD-IPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 DDYVPDKKECSKYWRC--VNGEGVQ--FSCQPGTIF 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                 294 TVVDDPAMHEDYAYYFPMNNIWCSYDHAASVVTKAEYAKSKGLAGTMVWSVETDDFRGLC 353
                                       234 RPGQIALGIPLYGRCWTLASQQETGYYAPAHQPGAAGDWTKSPGMLGYNEICYMQTTQDW 293
                                                                                                                                                                       388 GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTPTTTPSPTTTTTSSP 447
                                                                                                                                                                                                                                                                                          377 -----PPLPTTRDPSEPTTTRAPPP----PG----------THC 403
                 TRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEW 330
                                                                                           331 HIQYDEYYNAPYGY---NDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC 387
                                                                                                                                                                                                                                                     448 TIPITIPSPITPITIPSPITPIPITPIPAPTISIPSPITTEHISBIPKYTIVVDGHLIKC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Kinshu x Showa; TISSUE=Integument;
Abdel-Banat B.M., Koga D.;
"Molecular cloning of Bombyx mori chitinase cDNA; a unique insert of 9
"Molecular cloning of Bombyx mori chitinase of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

E MBL; AB052914; BAB20017.1;

EMBL; AB052914; BAB20017.1;

E MGO; GO:0005576; C:extracellular; IEA.

GO; GO:000576; F:chitin binding; IEA.

GO; GO:0016798; F:hydrolase activity; IEA.

GO; GO:0016798; F:hydrolase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR001223; Glyco_hydro_18.

R InterPro; IPR001223; Glyco_hydro_18AS.

R Pfam; PF01007; GBM 14; 1.

R Pfam; PF01007; GBM 14; 1.

R Pfam; PF000704; Glyco_hydro_18; 1.

R Pfam; PR00704; Glyco_hydro_18; 1.

R SNART; SM00494; ChtbD2; 1.

R PR05TER; SM00494; ChtbD2; 1.

R PR05TER; SM00516; GHITINASE 18; 1.
                                                                                                                                                                                                                                                                                                                                508 YKEGDIPHPINIHKYLVCEF-VNGGWWVHIMPCPPGTIMCQEKLTC 552
                                                                                                                                                                                                                                                                                                                                                      404 TILGINPDPLDCTHYYLCSINTSGGFDEKEEVCPEGTLFNPQSFYC 449
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Last sequence update)
Last annotation update)
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Matches 207; Conservative
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Bombyx mori (Silk moth)
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NCBI_TaxID=7091;
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                                                                                                                                                                                                           DLCTHILYSPIGVTEKSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDVKFMVAVGG 105
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                                                                                                                                                                                                                                             WYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 TRTTARPTT-----TTTKVPHGTTEDPDINVRPEVEELPT-ENEVDNADV-CNSE 492
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Neopiera, Endopeerygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
Bombycidae, Bombyx.
NCBI_TaxID=7091;
                                                                                                                                                          WAEGGSKYSHWVAQKSTRMSFIRSVVDFLKKYDFDGLDLDWEYPGAADRGSFSDKDKFL
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                                                                                                                                                                                                                                                                                              ALVRELKDAF -- EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
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EMBL; U86876; AAB47538.1; -.
                                                                                       27.0%; Score 837.5; DB 5; Length 543; llarity 35.9%; Pred. No. 2.1e-44; Conservative 78; Mismatches 208; Indels 83
                                                 21 543 CHITINASE.
543 AA; 60982 MW; DE29675D83AEC2EF CRC64;
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               18; 1.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE_18
Glycosidase; Hydrolase; Signal
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Bombyx mori (Silk moth)
                                                                                                    Local Similarity
les 207; Conserv
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SEQUENCE FROM N.A.
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459 PITIPSPITPTPTPTPTPAPTTSTPSPITIE-----HTSETPKYTTYVDGHLIKCYKE 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 WYEGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 ADVHSPLYKRPHD-QWAYEKLNVNDGLNLWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 GLGTYINKEAGGGDPAPYTNATGF-----WAYYEICTEVDADGSGWTKKWDEFGKCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 FKCTHLMYGFAKIDBYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0008061; F:chitin binding; IEA.

GO; GO:0008061; F:chitin binding; IEA.

R GO; GO:0005975; P:carbolydrate metabolism; IEA.

GO; GO:0005975; P:carbolydrate metabolism; IEA.

R InterPro; IPR001257; Chitin bind PerA.

R InterPro; IPR001257; Chitin bind PerA.

R InterPro; IPR001579; Glyco_hydro_18.

R InterPro; IPR001579; Glyco_hydro_18.

R Pfam; PF01607; CBM_14; 1.

R Prodow; D000041; Glyco_hydro_18; 1.

R PROSITE; SM00494; ChtBD2; 1.

R SWART; SM00636; Glyco_18; 1.

R PROSITE; PS01095; CHITINASE_18; 1.

R PROSITE; PS01095; CHITINASE_18; 1.

R SEQUENCE 565 AA; 63394 MW; 77D26D014875F3B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG9307 protein (LP08894P).
CG9307, melanogaster (Fruit fly).
Bursophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score bo....
35.9%; Pred. No. 2.2e-44;
rive 78; Mismatches 208; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Embydracida Endoprerygota Diptera: Brachycers: Muscomorpha;

Embydracida Endoprerygota Diptera: Brachycers: Muscomorpha;

Embydracida Endoprerygota Diptera: Brachycers: Muscomorpha;

Embydracida Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress Endopress E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 RINEGYHVPELCEALDAIHAMTYDLRGNWAGFADVHSPLYKRKHD-QYAYEKLNVNDGLA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377
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MEDLINE=20196006; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Hölt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 SDQASRIVCYFSNWAVYRTGIGRYGLEDVPADLCTHIIYSFIGWNDKSWDVLVIDPELD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 LWEEMGCPANKLVVGVPFYGRTFTLSNSNKNYNMGTYINKEAGGGAPGPYTNASGFLAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 TTTTTTTTPAP---EKSTEEPEEVVYPVDPVEPTDPEQPMGPQFDPNEIDCTNRDFVPHP
                                                                                                                                                                                                                                                                              88 NHNSWEKRGYERFINILRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFL
                                                                                                                                                                                                                                                                                                                                                                                                                   148 QEYKFDGLDLDWEYPGS--RLGNPKIDKQNYLALVRELKDAF--EPHGYLLTAAVSPGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 IDMDDFHGMCGRKNGLIQILYDNMKN------YRVPEPTRQTIPRPEWAKPPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 TPAPTISTPSPTTTEHTSETPKYTTY--------VDGHLIKCYKEGDIPHP
                                                                                                                                     SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPPKCTHLMYGPAKIDEYKYTIQVFDPYQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 LENDDFKGHCGPKNPLLNKVH-NMINGDEKNSFECILGPSTTTPTFTTP----TTPTTT
                                                                      Gaps
                                                                      87;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
       Length 595;
                                                                      Indels
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Last sequence update)
Last annotation update)
27.0%; Score 837.5; DB 5; 35.2%; Pred. No. 2.3e-44; ive 84; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 INIHKYLVCEFVNGGWWVHIMP----CPPGT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 -NCRKYFRC-----VHGKPVEFECKEGT 562
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
       Query Match
Best Local Similarity 35.2'
Matches 201; Conservative
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Q9W2M7
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59 --KCAYDRFTALKQQNANLKAILAVGGWNEGSPKYSKMAADPVLRNRFITSSIELLKKHG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 ESPSEGFSCPADA-----PAGYIRDPDNCSKFYYC----SGGKTHNFDCPSGLNFDLDT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .52 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDI 211
      235 QQQLMVDAVVKYWLKAGAPAEKLILGVPFYGRSFTLATAEGNQPGAPHIGKGIAGNYSRE 294
                                                                                                                                                                                                                                               373 VMVWSLENDDFKGHCGPK-NPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTT 431
                                                                                                                                                                                                                                                                                                                                                                               -----NTPSGLTTESNR 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 ETPK--YTTYVDGHLIKCYKEGDIPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEK 549
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"Cloning and characterization of a cDNA encoding a chitinase from hepatopancreas of the Penaeus vanameii (Crustacea, Decapoda).";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF1315699; AANTAGATI!
R GO; GO:0006576; C:extracellular; IEA.
R GO; GO:0016787; F:rhitin binding; IEA.
R GO; GO:0016787; F:rhydrolase activity; IEA.
R GO; GO:0016787; F:rhydrolase activity; IEA.
R GO; GO:0016787; F:rhydrolase activity; IEA.
R GO; GO:000630; P:chitin metabolism; IEA.
R InterPro; IPR001579; Glyco_hydro_18AS.
R Ffam; PF010704; Glyco_hydro_184; 1.
R Ffam; PF010704; Glyco_hydro_18; 1.
R Frobom; P0000471; Glyco_hydro_18; 1.
R SWART; SM00649; ChtBD2; 1.
R SWART; SM00649; CHTBD2; 1.
R ROSTIE; PS01099; GHTINASE_18; 1.
R ROSTIE; PS01099; GHTINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 WEKRGYERFINILRIKNPELITMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD--DNHNS
                                                                                                           BGVLSY1ELCQLFQKEEWH1QYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSG
                                                                                                                                                    295 PGVLGYNELCEMMEREEWTQKWEATQQVPYAYRQRQWVGYEDPRSLALKAQYVWDNHLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Litopenaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 26.8%; Score 831.5; DB 5; Length 467; al Similarity 34.2%; Pred. No. 4.1e-44; 180; Conservative 87; Mismatches 174; Indels 85;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       388
                                                                                                                                                                                                                                                                                                                355 IMIWSLESDDFRGTCGQQPYPLLHEINRVLFGG----
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gurtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.W., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hortin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
Nelson D.R., Nollmon N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Shue S.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
RA Sher B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Weinsch C., Stapen M., Weissenbach J. Q.,
RA Williams S.M., Woodage T., Weinsey K.C., Wu D., Yang S., Yao Q.A.,
RA Kenner K.R., Remington K., Stungen M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Weinsey K.C., Wu D., Yang S., Yao Q.A.,
RA Kenner K.H., Zhong F.N., Reinger M., Zhou X., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Typeace; Feguratorson, Controller, IEA.

R GO; GO: 0005576; C:extracellular; IEA.

R GO; GO: 0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

R GO; GO: 0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

R GO; GO: 00056975; P:carbohydrate metabolism; IEA.

R GO; GO: 0006497; P:protein folding; IEA.

R GO; GO: 0006497; P:protein folding; IEA.

R InterPro; IPR001129; REBP_PFIASE.

R InterPro; IPR001129; REBP_PFIASE.

R InterPro; IPR001123; Glyco_hydro_18.

R InterPro; IPR001579; Glyco_hydro_18.

R Ffam; PF01607; CBM 14; 1.

R ProDom; PD00044; Glyco_hydro_18; 1.

R ProDom; PD00044; Glyco_hydro_18; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51055 MW; BEF4F126F1DD8D9B CRC64;
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PROSITE, PS00453, FKBP_PPIASE 1, 1.
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HSSP; P07254; 1CTN.
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SMART; SM00636; Glyco_1
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151

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Gaps

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175	270	330	293 387	353	447	376	507	403			
	** KELNKI-POHMAYWIYDYHGGWENFYGHNAPLYKRP-DETDELHTYFNVNYIMHYYLNNGA		RPGQIALĞIPLYGRCI HIQYDEYYNAPYGY-	1	GPKNPLLN	: :::	S TTPTTTPSPTTTPSPTTPTPTPTPAPTTSTPSPTTTEHTSETPKYTTVVDGHLIKC	7PELPITTRDPNEPTTTRAPPPPGPGPTTRAPPP	8 YKEGDIPHPINIHKYLVCEF-VNGGWWVHIMPCPPGTIWCQEKLTC 552	4 TOPGLNPDPLDCTHYYLCSLNTSGGYNEKBEVCPEGTLYNPQSYYC 449	
117	212	271	234	294	388	354	448	377	508	404	
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Search completed: March 22, 2004, 06:59:24 Job time : 113.679 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein

March 22, 2004, 06:30:23 ; Search time 168.752 Seconds (without alignments) 929.256 Million cell updates/sec Run on:

US-09-662-293-15

score:

3107 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCOEKLTCIGE 555 Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* Database

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay52523 House dus	Aau96327 Der HMW-m	Aau96328 Der HMW-m	Aay52525 House dus	Aau96329 Der HMW-m	Aay52533 D. pteron	Aau96337 Der HMW-m	Aau96338 Der HMW-m	Aay52535 D. pteron	Der	Abp72636 Anopheles		_	Aab07183 Manduca s	Abp72619 Manduca s		Арр72625 Вотруж то		Abb64366 Drosophil	Aae28197 Flea chit		Aae28199 Flea PCfC	Abp72635 Aedes aeg	3 Chelon	Abp72626 Hyphantri
SUMMARIES	QI QI	AAY52523	AAU96327	AAU96328	AAY52525	AAU96329	AAY52533	AAU96337	AAU96338	AAY52535	AAU96339	ABP72636	ABB58595	AAW01824	AAB07183	ABP72619	ABP72634	ABP72625	ABB71737	ABB64366	AAE28197	AAE28203	AAE28199	ABP72635	ABP72633	ABP72626
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This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides

Aaw08584 Human 50	Aaw40259 Human chi	25 MO-21	Aae00432 Human chi	903 Human	291 Huma	Abu09914 Partial m	ŭ	Adc24231 Human NOV	Adc51464 Chitotria	Aaw08585 Human 39	7 Human	Aaw40260 Human chi	Aay42426 MO-13B cl	Aae00433 Human chi	4 Human	Abb76292 Human chi	Aaw31498 Human chi	544 Amino	Abp72621 Human chi
AAW08584	AAW40259	AAY42425	AAE00432	AAE25903	ABB76291	ABU09914	ABR55543	ADC24231	ADC51464	AAW08585	ADC24237	AAW40260	AAY42426	AAE00433	AAE25904		AAW31498	ABR55544	ABP72621
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26	27	28	29	30	31	32	33	34	35	36	37		3						45

ALIGNMENTS

RESULT 1

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Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                           House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-052700/04.
N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
                                                                                                                                                                                                             . .19
'note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 111-113; 154pp; English.
                                                                                                                                                                              Location/Qualifiers
        AAY52523 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Mccall CA, Hunter SW, Weber ER;
                                                                                                                                                                                                                                                                                                              98US-00062013.
98US-0085295P.
98US-0098909P.
                                                                                                                                                                                                                                                                                          99WO-US008524.
                                                     (first entry)
                                                                                                                                                       Dermatophagoides farinae.
                                                                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                               17-APR-1998;
13-MAY-1998;
02-SEP-1998;
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                                                                                                                                                                                                                                                                                         16-APR-1999;
                                                     22-FEB-2000
                                                                                                                                                                                                                                                                   28-OCT-1999
                               AAY52523;
                                                                                                                                                                                       Peptide
                                                                                                                                                                                                             Protein
AAY52523
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HMW-map, American house dust mite, antiallergic; mite, IgE; a allergenic protein; immunoglobulin E; hypersensitivity;

Dermatophagoides farinae immunocomplex formation.

WO200222807-A2 21-MAR-2002

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farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids enroding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, tragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as
                                                                                                                                                                                                                                                                                                                                                                                                  allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 555 AA;
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14-SEP-2001; 2001WO-US028730

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   Length 555;
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100.0%; Score 3107; DB 3; 100.0%; Pred. No. 1.8e-217;
                                0; Mismatches
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AAU96327 standard; protein; 555

Der HMW-map polypeptide #14

(first entry)

15-JUL-2002

AAU96327

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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a readent comprising a nonpresing by the protein. The protein or a readent comprising a noncation is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the confount of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing Mypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention
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100.0%; Pred. No. 1.8e-217;
ive 0; Mismatches 0;
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Der HMW-map protein, useful as a vaccine f
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                                                                                                                                                                                                                                                                                                   Weber ER;
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Best Local Similarity 100.
Matches 555; Conservative
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N-PSDB; ABK69571.
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for aliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonprotein assemblishe to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The MW-map protein can be used in the city immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AMU96314-AAU96342 represent Der HWW-map polypeptides of the invention
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                               KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
                                                                                                                                                               TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP
Der HMM-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
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N-PSDB; ABK69573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPINIHKYLVCEFVNGGWWVHIMPCP
                 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                                                                      181 RELXDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                                                  KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDBYYNAPYGYNDKIWVGYDDLASISC
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                                                  CTHLMYGRAKIDBYKYTIQVFDPYQDDNHNSWEXRGYERFNNIRLKNPELTTMISLGGWY
                                                                                                        EGSEKYSDWAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                                            RELKDAFREPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNWTYDYHGGWENFYGHNA
                                                                                                                                                                                                                PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
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 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             House dust mite (D. farinae) mite allergen protein (map) PDerf98-536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY52525 standard; protein; 536 AA.
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Claim 3; Page 125-127; 154pp; English
WPI; 2000-052700/04.
N-PSDB; AAZ38579, AAZ38580.
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Sequence 536 AA,

199 259 240 319 379 439 499 480 139 120 180 300 360 420 79 9 PGKDKI DRAYD I KELNKL FDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 181 PGKDKIDRAYDIKELNKIFDWMVWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN YTMHYYLINNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE **ELCOLFOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE** NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTPTTPSPT 20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 80 VFDPYQDDNHNSWEKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 241 YTWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 421 TPTTTPSPTTPTTPSPTTPTTPSPTTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI SLGGWYEGSEKYSDMAANPTYRQQF VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555 536 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE .; 0 Length 536; 97.0%; Score 3014; DB 3; 100.0%; Pred. No. 1e-210; iive 0; Mismatches 0; 536; Conservative Similarity 140 200 260 320 440 Query Match Best Local ò 엄 ò ద ò g 8 셤 ò 임 8 В 8 임 ò 유 8

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Dermatophagoides, designated Der MRW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein or a reagent comprising a non-proteinscens epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VFDPYQDDNHNSWEXRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                  use dust mite; antiallergic; mite; IgE; immunoglobulin E; hypersensitivity;
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                                                                                                                                                                HMW-map, American house
e allergenic protein; imm
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                                                                                                                                                                            This sequence represents Dermatophagoides farinae mite allergen protein

(map) PDerf98-536, the macure form of PDerf98-555 (AAY55523). PDerf98-536

has a molecular weight of 98 kD, comprising 536 amino acids, and is a

component of the Dermatophagoides farinae high molecular weight mite

allergen protein (HWM-map) composition. The HWM-map composition was

isolated from a D. farinae homogenate by gel filtration, with each

fraction being analysed for the presence of proteins that bound to IgE

present in mite-allergic dog antisera. Mite allergenic proteins and

peptides, and nucleic acids encoding them, may be used in therapeutic

compositions to modify an animal's hypersensitivity reaction to mite

allergens. Animals that may be treated include mammals and birds,

specially felines, canines, equines, humans, other pets, and work or

allergies via a skin test. The proteins and peptides can also be used to

raise antibodies, which have a variety of potential uses. For example,

recover desired dust mite allergens from a mixture of proteins
                                                                Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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AAU96329 standard; protein; 536 RESULT 5 AAU96329 ID AAU9

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                                                                                                                                                                                                                                                                                                                                                                                               Mite allergen protein; map; high molecular weight; HWW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
                         . high molecular weight Dermatophagoides nucleic acid polypeptides to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                    VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE
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/note= "Signal peptide'
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modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                         509;
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                                                                                                                                                                                                       81.8%; Score 2542; DB 3; I
81.7%; Pred. No. 2e-176;
ive 24; Mismatches 26;
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Best Local Similarity
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                         TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM
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                                                                                                                                                                           AAU96338 standard; protein; 509 AA.
                                                                                                         492 DCPKGTRWHATLKNCIQE 509
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                                                                              PCPPGTIWCQEKLTCIGE
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421 TPTTPSTTSTTPT--
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immunocomplex formation.
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                                                                                                                                                                                                                                                                                The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWM-map protein, and its related nucleic acid. The Der HWM-map protein is useful for aliciting an immune response against Der HWM-map protein. The protein or a reagent comprising a nonprotein sousceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A letter allergic response to a mite. A letter of a mite and inhibition allergic response to a mite. The DNA and protein can be used in the allergic response that bind to DnA and protein can be used in the cettion of anti-Der HWM-map protein activity associated with a disease. Antibodies that bind to Der HWW-map protein activity associated with a binding of proteins to IgE, to prevent immunocomplex formation, thus be binding bypersensitivity response to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96312
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                                                                                                                                                                                                                   mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                            12; Page 134-136; 161pp; English.
                                                                                                                                                   ER;
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                                                                 14-SEP-2001; 2001WO-US028730
                                                                                            14-SEP-2000; 2000US-00662293
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonprotein. The protein or a reagent comprising a noncrease spitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to a allergic response to a mite. The DNA and protein can be used in the cherapeutic dati-der HWM-map antibodies in animal fullids, and inhibition of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a disease. Antibodies that bind to Der HWM-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWM-map polypetides of the invention
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Der HMW-map, American house dust mite; antiallergic; mite; I;
mite allergenic protein; immunoglobulin E; hypersensitivity;
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-heg 26; Indels
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81.7%; Pred. No. 2e-176;
ive 24; Mismatches 26;
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Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Weber ER

SW,

Hunter

Mccall CA,

N-PSDB; AAZ38589, AAZ38590.

WPI; 2000-052700/04

Claim 3; Page 147-149; 154pp; English.

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This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 has brotein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 miles as molecular weight of 98 kD, compressing and has a high degree of homology with the D. farinae mature 98 kD allergen, mapB (AAY52525). Nucleic acid molecules encoding PDerp9-490 were isolated from a D. pteronyssius cDNA ilbrary by hybridisation with a probe encoding the D. farinae high molecular weight map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fagments may be used to diagnose allergies antibodies, which have a variety of potential uses. For example, they can be used as vacines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                        ---PITTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mite allergen protein, map, high molecular weight; HMW-map, allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy, treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                            KGMSPPGFITGEEGVLSYIELCQLFQXEEWHIQYDEYNNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                                        KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYBCLLGPSTTTP
              CTHLMYGFAKI DEYKYTI QVFDF FODDNINSWEKHGYERFINILRLKNPELITMI SLGGWY
                                                                                 EGSEKYSDMAANPIYRQOFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV
                                                                                                                                                                       PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                                                                                                                KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                        KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
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                                                                                                                                                                                                                                                                                                                                                                                                         TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM
                                                        EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                               RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNA
CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
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/note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 PCPPGTIWCQEKLTCIGE
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13-MAY-1998;
02-SEP-1998;
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22-FEB-2000
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183 KDKIDVAYELKELNQLFDWMNVYTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
                                                                                                                                                                                                                    DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTFTTPTTTTTTTFTTPSPTTP 441
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                                                                                                                                                          3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGPAKIDEYKYTIQVF 62
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                                                                                                                                                                                                                                                                                                        SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG
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                                                                                                                            22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                      Gaps
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                                                                                   52;
                                           Length 490;
                                                                                      21; Indels
                                      79.7%; Score 2475; DB 3;
ilarity 82.5%; Pred. No. 1.5e-171;
Conservative 21; Mismatches 21;
                      Query Match
Tocal Similarity
Sequence 490 AA;
                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insecticide, pesticide, insect control, insect; toxin; chitinase; enzyme; neuropeptide; transgenic plant; crop protection; mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the mosquito Anopheles gambiae chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein useful for combating insect pests, comprises a
translocating moiety comprising a plant protein capable of acting as a
carrier to translocate toxic moiety inside plant pathogen, and a toxic
                                                                                                                                                                                                                                                                      GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 490
                                                                               303 CQLFQKEEWHIQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGYSGVKHWSLEND
                                                                                                                                                        DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTFTTPSTTSTTTPT-----
                                                                                                                                                                                                         ----PTTTDSTSETPKYTTYID
                                                                                                                           DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTPTTPSPTTP
                                                                                                                                                                                       COLFOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND
MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL
                                                                                                                                                                                                                                                   GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "possible trypsin activation site"
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150. .157
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 ABP72636 standard; protein; 525 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae chitinase
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N-PSDB; ABZ81875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae.
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 262
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated mite allergenic protein of bermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein is useful for eliciting an immune response proteinaceous epitope is useful for identifying an animal (e.g., dog, proteinaceous epitope is useful for identifying an animal (e.g., dog, that) suseptible to or having an allergic response to a mite. A description is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map antibodies in animal fluids, and inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of immunoglobulin (Ig) E or Der HWM-map protein activity associated with a disease. Antibodies that bind to Der HWM-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWM-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                                         HMW-map, American house dust mite, antiallergic; mite, IgE; allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.7%; Score 2475; DB 5; Length 490; 82.5%; Pred. No. 1.5e-171; ive 21; Mismatches 21; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 144-146; 161pp; English.
                AAU96339 standard; protein; 490 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                Weber
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                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-00662293
                                                                                                           Der HMW-map polypeptide #26
                                                                            (first entry)
                                                                                                                                                                                                       Dermatophagoides farinae.
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                                                                                                                                                                          immunocomplex formation
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                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP.
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N-PSDB; ABK69585.
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                                                                                                                                                                                                                                      WO200222807-A2
                                                                            15-JUL-2002
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Drosophila melanogaster.

WO200171042-A2

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This protein is used in claimed fusion proteins of the invention. Such fusion proteins comprise a translocating moiety and a toxic moiety, where the translocating moiety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an insect-derived peptide or protein capable of causing deleterious effects on growth, development, protein capable of causing deleterious effects on growth, development, proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polynucleotides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease and analogues in protein is target-specific, and resists
                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
                                                                                                                                                                                                                                                                                                                                            YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                       YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 TPTTPTTTPSPTTPTTPSPTTPSPTTPSPTTTPSPTTPTPTPTPTPTPTPTPTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 APTT----STVAPGTITTPTGANPGTIQPPT--SDAPNHTITSTTTEGNPGTIRPPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 ITTEHTSEIPKYITYVDGHLIKCY--KEGDIPHPINIHKYLVC------EFVNGGWWVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LSIMACIGLMNASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM
                                                                                                                                                                                                                                                         59,
                                                                                                                                                                                                                           Length 525;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                      93; Mismatches 187;
                                                                                                                                                                                                                           32.5%; Score 1008.5; DB 38.4%; Pred. No. 7.7e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB58595 standard; protein; 4498 AA
                                                                                                                                                                 degradation in the insect gut
                                                                                                                                                                                                                                       Local Similarity 38.4 les 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 IMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---CPPGTLF
                                                                                                                                                                                               Sequence 525 AA;
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Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster polypeptide SEQ ID NO 2577

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTLFLLCALAYCI -----ONEASSEG-RVVCYYTNWSVYRPGTAKFNP---ONIN 77
                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 NYAQEVQELRAEFEREAEKTGRTRLLLTMAVPAGIEYIDKGYDVPKLNKYLDWFNVLTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867 AYRRNOWVGYDDEALVRKKAEYVVAQGLGGIMFWAIDNDFRGTCNGKPYPLIEAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHGGWENFYGHNAPLYKRPDETDELHTY---FNVNYTWHYYLNNGATRDKLVMGVPFYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFKCTHLMY---GFAKIDBYKYTIQVFDPYQDDNHNSWEKRGYERFINLLRLKNPELTTMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE-EWH-IQYDEYYNAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Mismatches 188; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 854.5; DB 4; Length 4498;
Pred. No. 2e-52;
                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English
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                                                                                                                                                                                                          EW,
                                                                                                                                                                                                          Myers
                                                                                                                                                                                                          PWD,
                                                                                             23-MAR-2001; 2001WO-US009231
                                                                                                                           2000US-0191637P.
2000US-00614150.
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Best Local Similarity 33.8'
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                                                                                                                                                                                                                                       2001-656860/75
                                                                                                                                                                         (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                         N-PSDB; ABL02698
                                                                                                                                                                                                                                                                                                                        interactions.
                                                                                                                           23-MAR-2000;
                                                                                                                                             11-JUL-2000;
                                                              27-SEP-2001
                                                                                                                                                                                                          Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An epidermal and gut chitinase (AAW01824) of Manduca sexta is encoded by CDNA clone 201 (AAT62557), isolated from a day-6 fifth instar whole larva cDNA library. The CDNA can be inserted into a vector for host expression of the chitinase protein, and may be utilised to control a population of insect petts. A recombinant baculovirus vector is provided for this purpose, as well as a transgenic tobacco plant that shows increased resistance to tobacco hornworm. Recombinant chitinase may also be expressed in host cells or larvae for subsequent purification and use as a biooide. The insect chitinase is expected to be more potent as an insect control agent than chitinases from other sources
                      522
-PSPTTPTPTTPTPAPTTSTPSPTTTEH 489
                                           TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG 542
                                                          plant; biological control; baculovirus; hookworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant contg. recombinant insect chitinase coding sequence useful for controlling plant pests.
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                     479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPTTPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corpuz L,
                                                                                                                                                                                              and gut chitinase
                                                                                                                                                                                                                                                                                                                                                                      'note= "proposed active site"
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/label= Conserved_region-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi HK,
                                                                                                                                                                                                                                                                                         . 19
|abel= Sig_peptide
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         'label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 37-40; 57pp; English.
                                                                                                                           Ą
                                                                                                                          AAW01824 standard; protein; 554
                                                                                                                                                                                              Manduca sexta larva epidermal
                                                                                                                                                                                                                    insect; transgenic insecticide; tobacco
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446 SPITPTITPSPITFIT-
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                                                                                                                                                                                                                                                                                                             . 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 554 AA;
                                                                                                                                                                                                                                                       Manduca sexta
                                                                                                                                                                                                                                                                                                                                                                                              WO9708944-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1995;
                                                                                                                                                                       27-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                            Active-site
                                                                                                                                                                                                                    Chitinase;
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                                                                                                                                                AAW01824;
                                             490
                                                                                                                                                                                                                                 biocide;
                                                                  523
                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                             Protein
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                                   124
                                                       56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110
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                                                                                                                           231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI
                                                                                                                                                                                                                                                                                                                          291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIBLCQLFQKEE--WHIOYDEYYNAPYGYNDKI
                                                                                                                                                                                                                                                                                                                                                                                                WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS
                                                                                                                                                                                                                                                                                                                                                                                                                     343 WYGYEDPRSVEIKMYWIKQKGYLGAMTWALDMDDFQGLCGEKNPLIKILHKHMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 -----SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDP1PTTTAKPASTTKTTVKTT
3 ATLATLAVLALATAV -----QSDSRARIV CYFSNWAVYRPGVGRYGIEDIPVEKCTHI
                                   MYGFAKI DEYKYTI QVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTIMI SLGGWYEGSE
                                                                                                                                                                             184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                                                                                                                                                  LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FECILGPSTYTPTPTTTPT-----TTPTTPS-----PTTPTTTPSPTTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 TIPITIPSPIT-----PIP-TIPIPAPITISIPSPITIBHISETPKYTTYVDGHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 TTTTAKPPQSVIDBENDINVRPEPKPEPQPEPEVEVP-PTENE------VDGSEI
                                                                                                         KYSDMAANPTYROOFIOSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Imaginal disc growth factor, IDGF; chitinase related protein; CHRP; tissue growth; wound healing; bone repair; cartilage repair; angiogenesis meat production; milk production; cancer; gene therapy; gut chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC
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20;

Gaps

Length 554; Indels 91; 64

6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL

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Query Match 27.0%; Score 838.5; DB 2; Best Local Similarity 35.4%; Pred. No. 1.9e-52; Matches 208; Conservative 79; Mismatches 210;

sexta chitinase.

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The present sequence is the protein sequence for the Manduca sexta gut chilinase. It was used to isolate the Drosophila melanogaster imaginal disc growth factor 4 (IDGF4) coding sequence. IDGF4 is a member of the chilinase related proteins (CHR9) and is involved in the promotion of cell growth, motility and morphogenesis. The gene and protein are expected to have mammalian homologues. They can be used in the treatment of cancer, wound healing, tissue regeneration following arthritis, osteoporosis, other skeletal disorders and burns, for revitalising scar tissue resulting from surgical procedures, irradiation, laceration, toxic chemicals, viral or bacterial infection or burns, to promote tissue growth during tissue engineering, for example tissues for skin graft replacements and bone regrowth, and to modulate the function of the female reproductive tract. In addition, they can also be used to increase meat, egg, sperm and milk production in animals. One possible method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVREL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKMPLLNKVHNMINGDEKNS 408
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                                                                                                                                                                                                                                                                                                                                                                                                                       91,
                                                                                                                                                                                                                                                                                                                                                                                  27.0%; Score 838.5; DB 3; Length 554; 35.4%; Pred. No. 1.9e-52; ive 79; Mismatches 210; Indels 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCYKEGD-IPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC
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                Disclosure; Col 53-58; 40pp; English.
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is by gene therapy
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ABP72619 standard, protein, 554 AA

(first entry)

11-JUN-2003

ABP72619;

ABP72619
ID ABP7
XX
AC ABP7
XX
DT 11-J

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The present sequence is that of Manduca sexta chitinase. This protein can comprise a translocating molety and a toxic molety, where the translocating molety is a plant a toxic molety, where the translocating molety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic molety is an insect-derived peptide or plant pathogen, and the toxic molety is an insect-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable insect peptides and proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polymucleotides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease are also provided. The fusion protein is target-specific, and resists
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                                         Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as a carrier to translocate toxic moiety inside plant pathogen, and a toxic
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                                                            neuropeptide; transgenic plant; crop protection
                                                                                                                                                                                                 85. .88
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                /note= "Asn is N-glycosylated"
545. .548
                                                                                                                                                                                                                                                                                                /note= "Asn is N-glycosylated"
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                                                                                                                                      l. .19
/label= Signal_peptide
                                                                                                                                                                     0. .554
label= Mature_protein
                                                                                                                      Location/Qualifiers
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303. .306
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Matches 208; Conservative
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Best Local Similarity
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                                                                                         Manduca sexta
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(ENVI-) DEPT
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170	.P 241	P 230	290	I 289	I 348	9 342	IS 408	- 396	ip 456	T 449	505	I 497			
1 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL	KDAF EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDW	RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP	LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAMSIED	1 LYKRPHD-QMAYEKLNVNDGLHLWEEKGCPSNKLVVGIPPYGKSFTLSAGNNNYGLGTFI	RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHI	0 NKEAGGGDPAPYTNATGFWAYYEICTEVDKDDSGWTKKWDEGGKCPYAYKGTQ	9 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS	WYGYEDPRSVEIKMWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKI	9 FECILGESTITETETIFITETTIPITESPITETITESPITETIFS	7SYTVPPPHTENTIPTPEWARPPSTPSDPSEGDPIPTTTAKFASTTKTTVKTT	7 ITPTTESPTTPTP-TTPTBAPTTSTPSPTTTEHTSETPKYTTYVDGHLI	0 TITTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENEVDGSEI	6 KCYKEGD-IPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLIC 552	- CNSDODYIPDKKHCDKYWRCVNGEAMQFSCOHGI	
111	184	171	242	231	291	290	349	343	409	397	457	450	506	498	
Dp	65	qo	ò	qq	δ	qq	à	Ор	ζ	DP	ò	Db	ò	qq	

Search completed: March 22, 2004, 06:51:45 Job time : 170.752 secs

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OM protein - protein search, using sw model

Run on:

March 22, 2004, 06:59:34; Search time 113.53 Seconds (without alignments) 1265.926 Million cell updates/sec

US-09-662-293-15 Title: Perfect score:

3107 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1049977 seqs, 258955339 residues Searched:

1049977 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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. cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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. cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
. cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
. cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 15, Appl	Sequence 18, Appl	Sequence 21, Appl	35,	38,	41,	Sequence 10, Appl	~	Sequence 4, Appli	4	6	14,	15,	Sequence 14, Appl	1, A
QI	US-10-218-743-15	US-10-218-743-18	US-10-218-743-21	US-10-218-743-35	US-10-218-743-38	US-10-218-743-41	US-10-004-219B-10	US-10-161-547-2	US-10-004-219B-4	US-10-161-547-4	US-10-004-219B-9	US-10-161-547-14	US-10-161-547-15	US-10-004-219B-14	US-10-004-219B-1
DB	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
* Query Match Length DB	555	555	536	509	509	490	445	466	473	466	452	373	373	455	476
% Query Match	100.0	100.0	97.0	81.8	81.8	79.7	23.8	23.8	23.7	23.6	23.5	23.2	23.2	22.8	22.8
Score	3107	3107	3014	2542	2542	2475	738	738	736.5	732	729.5	721.5	721.5	708.5	708.5
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Sequence 6743, Ap Sequence 632, App Sequence 1900, Ap Sequence 45, Appl Sequence 270, Appl	Sequences Sequences Sequences Sequences	sequent sequen	Sequence 33 Sequence 2, Sequence 18 Sequence 11 Sequence 19	Seguen Seguen Seguen Seguen Seguen	Sequence 12 Sequence 30 Sequence 82 Sequence 55 Sequence 55
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ALIGNMENTS

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GREERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: Maber, Exit R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 2002-08-13
FRIOR APPLICATION NUMBER: US/09/292,225
FRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0;
Sequence 15, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
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US-10-218-743-18

WE-10-218-743-18

WEDDIGATION NO. US20030096779A1

GENERAL INFORMATION:

APPLICANT: WCCall, Catherine A.

APPLICANT: Water, Shirley W.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVER: US/09/29, 225

PRIOR APPLICATION NUMBER: US/09/29, 225

PRIOR FILING DATE: 1998-09-02

PRIOR FILING DATE: 1998-09-03

PRIOR PILING DATE: 1998-04-17

PRIOR PELICATION NUMBER: 09/062, 013

PRIOR PELICATION NUMBER: 09/062, 013

PRIOR PELICATION NUMBER: 09/062, 013

PRIOR PELICATION NUMBER: 09/062, 013

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100.0%; Score 3107; DB 14; Length 555;
Best Local Similarity 100.0%; Pred. No. 3e-220;
Matches 555; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: Mutner, Shirley Wu
APPLICANT: Whenter, Exic R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PRO'
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2.C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT PILING DATE: 1999-04.15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR PILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-21
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Publication No. US20030096779A1
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Length 536;

DB 14;

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US-1U-LBW-141-38

US-1U-LBW-141-38

Sequence 38, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:

APPLICANT: Muncer, Shirley Wu
APPLICANT: Muncer, Shirley Wu
APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL 2032-08-13

PRIOR FILING DATE: 1998-09-04-15

PRIOR PELICATION NUMBER: 60/098,909

PRIOR FILING DATE: 1998-09-04-15

PRIOR FILING DATE: 1998-04-17

PRIOR PELICATION NUMBER: 60/098,565

PRIOR PELICATION NUMBER: 60/098,565

PRIOR PELICATION NUMBER: 09/062,013

PRIOR FILING DATE: 1998-04-17

PRIOR PELICATION NUMBER: 09/062,013

PRIOR FILING DATE: 1998-04-17

SOFTWARE: PALECATION NUMBER: 09/062,013

PRIOR FILING DATE: 1998-04-17

SOFTWARE: PALECATION NUMBER: 09/062,013

PRIOR PILING DATE: 1998-04-17

BRIOR PILING DATE: 1998-04-17

BRIOR PILING DATE: 1998-04-17

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                                                                                                                             1 MXTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
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                                                                         1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
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      52;
   Indels
      26;
      Mismatches
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-38
      24;
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| Sequence 35, Application US/10218743
| Publication No. US2003009677941
| Publication No. US2003009677941
| Publication No. US2003009677941
| GENERAL INFORMATION:
| APPLICANT: HUNCEL Shirley Wu
| APPLICANT: HUNCEL Shirley Wu
| APPLICANT: HUNCEL Shirley Wu
| APPLICANT: Waber, Eric R. |
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
| FILE REPERENCE: AL-2-C3
| CURRENT APPLICATION NUMBER: US/09/292,225
| PRIOR APPLICATION NUMBER: 60/098,909
| PRIOR FILING DATE: 1999-04-15
| PRIOR PELICATION NUMBER: 60/098,565
| PRIOR PELICATION NUMBER: 60/098,565
| PRIOR PELICATION NUMBER: 60/098,565
| PRIOR PELICATION NUMBER: 09/662,013
| PRIOR APPLICATION NUMBER: 09/662,013
| PRIOR PELICATION NUMBER: 09/662,013
| PRIOR PELICATION NUMBER: 09/662,013
| PRIOR PELICATION NUMBER: 09/662,013
| PRIOR PELICATION NUMBER: 09/662,013
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                                                                                                            20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ
                                                                                                                                                                       1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ
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Pred. No. 1e-178;
                                         0; Indels
   ; Pred. No. 2e-213; 0; Mismatches 0
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81.7%;
   100.08;
Best Local Similarity 100.
Matches 536, Conservative
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Sequence 41, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: Meber, Eric R.

TITLE OF INVENTION: NOVEL DEMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DEMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/09/292,225

PRIOR APPLICATION NUMBER: 60/098,909

PRIOR FILING DATE: 1998-09-02

PRIOR FILING DATE: 1998-04-15

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PALENTIN VORBER: 09/662,013

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

SEQ ID NO 41

LENGTH: 490
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                                                                                                                                                                                                                                                       EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
                                                                                                                                                                                                                                                                                          EGSEKYSDMAANPTYROOFVOSVLDFLOEYKFDGLDLDWEYPGSRLGNPKIDKONYLTLV 180
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                                                                                                                      MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                                                                                                                                         CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
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                                                                                              1 MKTIYAILSIMACIGLANASIXRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                          Gaps
                                                        52.
                      Length
                                                        Indels
                  Query Match 81.8%; Score 2542; DB 14; Best Local Similarity 81.7%; Pred. No. 1e-178; Matches 456; Conservative 24; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 TPTTPSTTSTTTPT-------
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APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boct, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: At use in therapy or prophylaxis against diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
TITLE OF INVENTION: ALS. 2183-51340S
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 201-11-02
SOFTWARE: PATCHING DATE: 201-11-02
SOFTWARE: PATCHING VET: 2.1
                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                            63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                      142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSPG
                                                                                                                                                                                                                                      3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                                                                                                                                                                                             82 DPYODDNEMSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIO
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                                                                                                                                                                                      22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDBYKYTIQVF
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                                                                                                                                  52;
                                                                                Length 490;
                                                                                                                                  Indels
                                                                          Query Match 79.7%; Score 2475; DB 14; Best Local Similarity 82.5%; Pred. No. 8.4e-174; Matches 443; Conservative 21; Mismatches 21;
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Pred. No. 5.3e-46;
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; ORGANISM: Dermatophagoides farinae US-10-218-743-41
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Best Local Similarity
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 158; Conservative
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                                                                                                                                                                 205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
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                                                                                                                                                                                                                                                                        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                                                                                                                                                                                                                                                                                                                                   325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
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                             34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                              385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTFTTTPTTFTTFTTPSPTTPTTT
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Gaps
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| Sequence 2, Application US/10161547
| Publication No. US20030143216A1
| GENERAL INFORMATION:
| APPLICANT: Gray, Patrick W.
| TITLE OF INVENTION: GHITINASE CHITIN-BINDING FRAGMENTS
| TITLE OF INVENTION: GHITINASE CHITIN-BINDING FRAGMENTS
| FILE REFERENCE: 27866/35407
| CURRENT APPLICATION NUMBER: US/10/161,547
| CURRENT FILING DATE: 1999-03-12
| PRIOR PILING DATE: 1999-03-12
| PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
| PRIOR PILING DATE: EARLIER FILING DATE: 1998-03-12
| NUMBER OF SEQ ID NOS: 39
| SOFTHARE: Patentin Ver. 2.0
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58;
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Mismatches 150; Indels
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85;
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Best Local Similarity 34.2
Matches 152; Conservative
Conservative
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US-10-161-547-2
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US-10-161-547-2
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APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.P.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REPERENCE: 2183 51360S
FILE REPERENCE: 2183 51360S
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT APPLICATION NUMBER: US/10/11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTING PATE: 201-11-02
SEQ ID NO 4
LENGTH: 473
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                                                                                                                                                                                                        325 FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAPLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                       134 TYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-- 191
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                                                                                                                                                                                                                                                                                                                                                                                  -----RYPLIQTLRQELSLPYLPSGT 394
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                                                                                                                                                                                                                                                                                                                             16 LANASIKADHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEY
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292 GAYTRQAGFWAYYEICTFLRSGATEVW----DASQEVPYAYKANEWLGYDNIKSFSVKAQ 347
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                                                                     364 FLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10161547
; Sequence 4, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERRINCE: 27866/35407
; CURRENT APPLICATION NUMBER: US/10/161,547
; CURRENT FILING DATE: 1999-03-12
; PRIOR PILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/039,198
; PRIOR PILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PACENTING DATE: AACHIER FILING DATE: 1998-03-12
; SOFTWARE: PACENTING DATE: AACHIER FILING DATE: 1998-03-12
; SOFTWARE: PACENTING DATE: AACHIER FILING DATE: 1998-03-12
; SOFTWARE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF THE PACENTIAL OF TYPE: ACCOUNTY OF TYPE: ACCOUNTY OF THE PACENTY OF TYPE: ACCOUNTY OF THE PACENTY OF TYPE: ACCOUNTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENTY OF THE PACENT
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23.6%; Score 732; DB 14; Length 466;
Best Local Similarity 33.9%; Pred. No. 1.6e-45;
Matches 151; Conservative 85; Mismatches 151; Indels 5
                                                                                                                                    348 WİKQNNFGGAMIWAIDLDDFTGSFCDQGKFPLTSTLNKA---
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US-10-161-547-4
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RESULT 11 US-10-004-219B-9

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                                                                                                   APPLICANT: MACIOZYME
APPLICANT: MACIOZYME
APPLICANT: Abris, Johannes M.F.G.
APPLICANT: Abris, Johannes M.F.G.
APPLICANT: Abris, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: WHICH WERE US/10/004,219B
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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| Sequence 14, Application US/10161547
| Sequence 14, Application US/10161547
| Publication No. US20030143216A1
| GENERAL INFORMATION:
| APPLICANT: Gray, Patrick W.
| APPLICANT: Tjoelker, Larry W.
| TILLE REPERENCE: 27866/33407
| CURRENT APPLICATION NUMBER: US/10/161,547
| CURRENT PILING DATE: 1999-03-12
| PRIOR APPLICATION WUMBER: US/09/267,574
| PRIOR APPLICATION WUMBER: EARLIER APPLICATION NUMBER: 09/039,198
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
| NUMBER OF SEQ ID NOS: 39
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23.5%; Score 729.5; DB 14; Length
Best Local Similarity 37.0%; Pred. No. 2.3e-45;
Matches 154; Conservative 69; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LUCATION: (1)..(452)
; OTHER INFORMATION: /note="Mouse AMCase"
US-10-004-219B-9
Sequence 9, Application US/10004219B Publication No. US20030087414A1 GENERAL INFORMATION:
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289 KGATKQRIQ-DQ--KVPYIPRDNQWVGFDDVBSFKTKVSYLKQKGLGGAMVWALDLDDFA 345
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      51 NDETLYQEFNGLKKMNPKLKTLLAIGGMNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 110
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APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
APPLICANT: Boot, Rolf G.
APPLICANT: Boot, Rolf G.
APPLICANT: Boot, Rolf G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: which mucus is involved or infection diseases
TITLE REPERENCE: 2183-51364
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                                                                                                                               205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                   265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL
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22.8%; Score 708.5; DB 14; Length
Best Local Similarity 35.9%; Pred. No. 8.1e-44;
Matches 149; Conservative 75; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)..(455)
; OTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10004219B Publication No. US20030087414A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (1).
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US-10-004-219B-14
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Publication No. US20030143216A1

GENERAL INFORMATION:

APPLICANT: Gray, Patrick W.

APPLICANT: Tjoelker, Larry W.

TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRACMENTS

FILE REFERENCE: 27866/35407

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT FILING DATE: 1999-03-12

PRIOR PLING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198

PRIOR PLING DATE: EARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39

SOFTHARE: PATENTIN VET. 2.0
                                                                                                                                                     DB 14; Length 373;
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                                                                                                                                              23.2%; Score 721.5; DB 14; ilarity 37.7%; Pred. No. 6.9e-45; Conservative 83; Mismatches 117;
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LENGTH: 373
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Best Local Similarity 37.74
Matches 136; Conservative
                                                                                 ; ORGANISM: Homo sapiens
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Search completed: March 22, 2004, 06:59:26 Job time: 113.679 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 22, 2004, 06:30:23; Search time 168.752 Seconds (without alignments) 929.256 Million cell updates/sec Run on:

Title: Perfect score:

US-09-662-293-18 3107 1 MKTIYAILSIMACIGIMNAS.....IMPCPPGTIWCOEKLTCIGE 555

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_29Jan04;*
1: geneseq11980s;*
2: geneseq11990s;*
4: geneseq12000s;*
5: geneseq12001s;*
5: geneseq12003s;*
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ALIGNMENTS

 19 "Signal peptide"
 55 "Nature PDerf98-555" Location/Qualifiers Key Peptide Protein

98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524 17-APR-1998; 13-MAY-1998; 02-SEP-1998; 16-APR-1999; W09954349-A2 28-OCT-1999

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2000-052700/04. N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 111-113; 154pp; English.

This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides

Der HMW-map; American house dust mite; antiallergic; mite; IgB; mite allergenic protein; immunoglobulin B; hypersensitivity;

Dermatophagoides farinae. immunocomplex formation.

WO200222807-A2 21-MAR-2002

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composition. The HWW-map composition was isolated from a D. farinae composition. The HWW-map composition was isolated from a D. farinae composition. The HWW-map composition was isolated from a D. farinae composition, with each fraction being analysed for the presence of proteins that bound to IgB present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids cancing them, may be used in therapautic compositions to modify an enimal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, thumans, other pets, and work or domestic animals. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
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New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.

ER.

Mccall CA, Hunter SW, WPI; 2002-351888/38.

N-PSDB; ABK69571

(HESK-) HESKA CORP

14-SEP-2001; 2001WO-US028730. 14-SEP-2000; 2000US-00662293 Claim 12; Page 114-116; 161pp; English.

The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related mucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonpresing a susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the determined anti-bot HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing Mypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU963142 represent Der HWW-map polypeptides of the invention ö 120 240 240 300 360 9 121 EGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 1 MKTIYAILSIMACIGLANASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY EGSEKYSDMAANPIYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA Gaps . 0 Indels Score 3107; DB 5;
Pred. No. 1.8e-217;
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AAU96327 standard; protein;

Der HMW-map polypeptide #14

(first entry)

15-JUL-2002

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                                                                        TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP
                                            Der HVW-map, American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
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                                                                                                                                                                                                                                                  PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                  CTHLMYGFAKI DEYKYTIQVEDBYQDDNHNSWEKRGYERFNNLELKNPELTTMISLGGWY
                                                                                                                                                                                  181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                         PLYKRPDSTDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                                                                                                                                                                KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                                    KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWYGYDDLASISC
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                                                                                                                                                                                                                                                                                                                                                                                                                       481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP
                                                                         CTHIMYGFAKIDEYKYTIQVFDFYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                             EGSEKYSDMAANPTYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                 121 EGSEKYSDWAANPTYRQOFIQSVLDFLQSVKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                                                  RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA
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MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVĞIWSVYHKVDPYTIEDIDPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGTIWCQEKLTCIGE
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02-SEP-1998;
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This sequence represents Dermatophagoides farinae mite allergen protein

(map) PDerf98-536, the mature form of PDerf98-555 (AAY5523). PDerf98-536

(map) PDerf98-536, the mature form of PDerf98-555 (AAY5523). PDerf98-536

(map) PDerf98-536, the mature form of PDerf98-555 (AAY5523). PDerf98-536

(map) PDerf98-536, the mature form of PDERF98-536 (AAY5523). PDerf98-536

(map) Popular weight of 98 KD, composition acids, and is a

allergen protein (HWM-map) composition. The HWM-map composition was

isolated from a D. farinae homogenate by gel filtration, with each

creation being analysed for the presence of proteins that bound to IgB

present in mite-allergic dog antisera. Wite allergenic proteins and

peptides, and nucleic acids encoding them, may be used in therapeutic

compositions to modify an animal's hyperensitivity reaction to mite

allergens. Animals that may be treated include mammals and birds,

compositions to modify an animal's equines, humans, other pets, and work or

allergens. Animals The proteins of tragmente may also be used to diagnose

allergies via a skin test. The proteins and peptides can also be used to

craise antibodies, which have a variety of potential uses. For example,

they can be used as vaccines to passively immunise animals against dust

mite hypersensitivity, as positive controls in test kits and as tools to

crecover desired dust mite allergens from a mixture of proteins
                                                                                            Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                             Claim 3; Page 125-127; 154pp; English.
                                 N-PSDB; AAZ38579, AAZ38580.
   2000-052700/04,
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Sequence 536 AA;

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                                                          20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ
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97.0%; Score 3014; DB 3; Length 536; 100.0%; Pred. No. 1e-210;
                              0; Indels
       100.0%; Prec. ...
                             Matches 536; Conservative
               Best Local Similarity
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AAU96329 standard; protein; 536 AA

RESULT 5
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related mucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonpresing by susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A the DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA map protein can be used in the disease. Antibodies that bind to Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IGB, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96312 represent Der HWW-map protein envention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ
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100.0%; Pred. No. 1e-210;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             14-SEP-2001; 2001WO-US028730.
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                                                                                                 Der HMW-map polypeptide #16.
                                                          (first entry)
                                                                                                                                                                                                                       Dermatophagoides farinae.
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                                                                                  420
                                                              439
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                                                                                                                                                                                                                                                                                                                   Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI
                     ELCQLPQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE
                                 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTPTTTPTTPSPT
                                                                           NDDFKGHCGPKNPLLNKVFNMINGDEKNSFECILGPSTTTPFTTFFTTFTTFFTFSFT
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                                                                                                                                                VDGHLIKCYKEGDIPHPTNIHKYLVCBFVNGGWWVHIMPCPPGTIWCQEKLICIGE
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                                                                                                                                                                                                                                                                                                 pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
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N-PSDB; AAZ38585, AAZ38586, AAZ38588.
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/note= "Signal peptide"
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02-SEP-1998;
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modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite allerge shypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
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mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                  Score 2542; DB 3; Length 509;
Pred. No. 2e-176;
4; Mismatches 26; Indels 53
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Best Local
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for allciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A learned of allergic response to a mite. A learned of allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map protein activity associated with a binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANUS6314-AAU96342 represent Der HWW-map polypeptides of the invention mite allergenic protein isolated from Dermatophagoides, designated HWW-map protein, useful as a vaccine for treating mite allergy. Claim 12; Page 134-136; 161pp; English. Weber ER 14-SEP-2001; 2001WO-US028730 14-SEP-2000; 2000US-00662293 Conservative Hunter SW, WPI; 2002-351888/38 Similarity (HESK-) HESKA CORP Sequence 509 AA; N-PSDB; ABK69581 WO200222807-A2 Best Local Sim: Matches 456; 21-MAR-2002 Mccall CA, 121 181 241 301 61 121 61 181 241 301 361 Query Match 8 8 8 ∂ g ò 셤 ठ a 8 심 8

240 420 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKIPDWMNVMTYDYHGGWENFYGHNA 240 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420 TPTTTPTTPTTPTTPSPTTPSPTTPSPTTTPSPTTPTTPSPTTPTPTPTPTPTPTPTPTPTPTPTS 480 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNIRLKNPELTTMISLGGWY 120 9 CTHIMYGFAKIDEYKYIQVPDPFQDDNHNSWEKHGYERPNNLRLKNPELTMISLGGWY RELKEAFEPFGYLLTAAVSPGXDKIDVAYELKELNQLFDWMVWTYDYHGGWENVFGHNA KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLINKVHNMINGDEKNSYECLLGPSTTTP 1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFK 1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 52; 81.8%; Score 2542; DB 5; Length 509; 81.7%; Pred. No. 2e-176; .ive 24; Mismatches 26; Indels 55 361 421

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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related mucleic acid. The Der HWM-map protein is useful for aliciting an immune response or acid. The Der HWM-map protein. The protein or a reagent comprising a nonpretained susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic anti-Der HWM-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a disease. Antibodies that bind to Der HWM-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU963142 7 9 9 ---PITTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKXLVCEYIATPNGGWWVHIM 491 New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy. 1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK TPSPITITEHISETPKYITYVDGHLIKCYKEGDIPHPINIHKYLVCEFV---NGGWWVHIM Gaps 52; 81.8%; Score 2542; DB 5; Length 509; 81.7%; Pred. No. 2e-176; ive 24; Mismatches 26; Indels 5; protein; immunoglobulin E; hypersensitivity; HMW-map; American house dust mite; antiallergic; Claim 12; Page 139-141; 161pp; English. AAU96338 standard; protein; 509 AA Weber ER; 509 552 14-SEP-2001; 2001WO-US028730. 14-SEP-2000; 2000US-00662293. PCPPGTIWCQEKLTCIGE 492 DCPKCTRWHATLKNCIOE Der HMW-map polypeptide #25. (first entry) Matches 456; Conservative 121 TPTTPSTTSTTPT--Dermatophagoides farinae. immunocomplex formation. Modall CA, Hunter SW, 2002-351888/38. Similarity (HESK-) HESKA CORP N-PSDB; ABK69583 allergenic Sequence 509 AA; WO200222807-A2. 15-JUL-2002 21-MAR-2002 Query Match AAU96338; 481 Local RESULT 8 8 g 챵 쉽 ò

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This sequence represents Dermatophagoides pteronyssius mite allergen

protein (map) Poerp98-490, the mature form of pDerp98-509. Poerp98-490

chas a molecular weight of 98 kD, comprising 490 amino acids, and has a high degree of homology with the D. farinae mature 98 kD allergen, mapB (CC (AAY52525). Nucleic acid molecules encoding poerp9-490 were isolated from a D. perconysius cDNA library by hybridisation with a probe cocding the D. farinae high molecular weight map (HMW-map) composition.

Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal; s hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, char pets, and work or domestic animals. The proteins and palso be used to diagnose allergies via skin test. The proteins and poptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively intest kits and as tools to recover desired dust mite appearance of intest kits and as tools to recover desired dust mite allergens from a little of proteins. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                               Claim 3; Page 147-149; 154pp; English.
 Weber ER;
                               WPI; 2000-052700/04.
N-PSDB; AAZ38589, AAZ38590.
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Matches 443; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PTTTDSTSETPKYTTYIDGHLIKCYKOGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust miter; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canlne; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                181 RELKEAPEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA
                                                                                                                                                                                                                   PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA
                                                                                                                                                                                                                                                                              KGMSPPGFITGEEGVLSYIELCQLFQXEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                                                                               KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHMMINGDEKNSYECLLGPSTTTP
                                                                                  EGSEKYSDWAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV
                                                                                                                                                                                            PLYKRPDETDELHTYFNVNYTWHYYLNNGATRDKLVMGVPFYGRAWSIBDRSKLKLGDPA
                                                                                                                                                                                                                                                           KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                                                                                                                           TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM
               CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY
                                                               EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                             RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                                                                                             KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
                                                                                                                                                                                                                                                                                                                                                                                                                              TPTTPSTTSTTTPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115. .117
/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
115. .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY52535 standard; protein; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCPPGTIWCQEKLTCIGE 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCPKGTRWHATLKNCIQE 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00062013.
98US-0085295P.
98US-0098909P.
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(first entry)
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Modified-site
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13-MAY-1998;
02-SEP-1998;
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22-FEB-2000
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61
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243 MHYYLANGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302
                                                     COLFOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
                                                                             303 CQLFQKEBWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362
                                                                                                          DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTFTTTTTTTTTTTTTPTTP 441
                                                                                                                           363 DFKGHCGPKYPLLINKVHNMINGDEKNSYECLLGPSTITPTPTTPSTTSTTTPT----- 415
                                                                                                                                                                 442 TITPSPITPTTPSPITTPSPITTPTPTPTTPTPAPTISTPSPITTEHTSETPKYTTYVD 501
                                                                                                                                                                                            502 GHLIKCYKEGDIPHPTNIHKYLVCEFV.---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
                                                                                                                                                                                                                                            MHYYLINNGATRDKI.VMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UYDU-) UNIV DURHAM.
[ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Batehouse JA, Fitches EC, Edwards JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . :19
|abel= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            ABP72636 standard; protein; 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2001; 2001GB-00019274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2002; 2002WO-GB003598
                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae chitinase
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; ABZ81875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003014150-A2
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                                                                                                                382
                                                                                                                                                                                                  416
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     262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                 ABP72636
                                                                                                                                                                                                                                                                                                                              CXSXLXBXXBXXBXBXBXBXBZBBBBBBBBX8XBXBXBXBXBXSX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for aliciting an immune response against Der HWW-map protein or a reagant comprising a nonproteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal to allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the city immunoglobulin (Ig) or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to Igs, to prevent immunocomplex, formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergens, hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map protein on the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDWAANPTYRQQFVQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDKIDRAYDIKELNKCFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                              Der HWW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.7%; Score 2475; DB 5; Length 490; 82.5%; Pred. No. 1.5e-171; Live 21; Mismatches 21; Indels 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 144-146; 161pp; English.
                       AAU96339 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                              Weber ER
                                                                                                                                                                                                                                                                           14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                       14-SEP-2000; 2000US-00662293
                                                                                                       Der HMW-map polypeptide #26
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443; Conservative
                                                                                                                                                                                         Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                              Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-351888/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                  (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK69585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 490 AA;
                                                                                                                                                                                                                     WO200222807-A2
                                                                            15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                   AAU96339;
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The present sequence is that of the mosquito Anopheles gambiae chitinase.
Insecticide, pesticide, insect control, insect, toxin, chitinase, enzyme, neuropeptide, transgenic plant, crop protection, mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as carrier to translocate toxic moiety inside plant pathogen, and a toxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401. .466
/note= "serine/threonine/proline-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "possible trypsin activation site"
150. .157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "possible trypsin activation site"
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Drosophila melanogaster.

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fusion proteins comprise a ranslocating moiety and a toxic moiety, where the translocating moiety is a plant protein (e.g. a lectin) capable of a cating as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an insect-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable insect peptides and metabolites and analogues. Polynucleotides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease are also provided. The fusion protein is target-specific, and resists degradation in the insect gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305
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                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                             FSAMAAAGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 EFDHYGLLLTAAVASVEFSAGVSYDIPRISKSFHFLNVMVYDMHGAWDSYCGINAPLYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LSIMACIGLANASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIBDIDPFKCTHLM
                                                                                                                                                                                                                                                                                                                  YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK
                                                                                                                                                                                                                                                                                                                                                                                                                        YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SADTIDRIGOINVNASIHFWLAQGCIGRKLVLGIPLYGRNFTLASAANTQIGAPTVGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APTT-----STVAPGTTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITEHISETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC------EFVNGGWWVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                    525;
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 2577.
                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                               93; Mismatches 187;
                                                                                                                                                                                                                                  32.5%; Score 1008.5; DB 38.4%; Pred. No. 7.7e-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB58595 standard; protein; 4498 AA.
protein is used in claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                Local Similarity 38.4
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                                                                                                                                                                                                       Sequence 525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-ell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGDEKNSFECILGPSTTTPTPTTTTTTTTTT--------TPSPTT---PTTTP
                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AIGGWNEASSRFSPLVASNERRQOFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 AYRRNOWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence for for for form part of the parinted specification, but was obtained in electronic form part of from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4498;
                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.5%; Score 854.5; DB 4; 33.8%; Pred. No. 2e-52;
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                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                                                                            23-MAR-2001; 2001WO-US009231
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nes 202; Conserv
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                               WO200171042-A2
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---PSPTTPTPTPTPAPTTSTPSPTTTEH 489
                                                                     999
                                                                                                                                                                                                                     plant; biological control; baculovirus; hookworm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gopalakrishnan B;
                                                              TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant contg. recombinant insect chitinase coding useful for controlling plant pests.
                      479 RPAVSSTQAPP--PSTTPKLTBAEGSSLYIGGRASTTPPPPTTPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corpuz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.0%; Score 838.5; DB 2; Best Local Similarity 35.4%; Pred. No. 1.9e-52; Matches 208; Conservative 79; Mismatches 210;
                                                                                                                                                                                                        Manduca sexta larva epidermal and gut chitinase.
                                                                                                                                                                                                                                                                                                                                                                                        'note= "proposed active site"
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/label= Conserved_region-I
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                                                                                                                                                                                                                                                                                                                                         /label= Mat_protein
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                  AAW01824 standard, protein; 554
                                                                                                                                                                                                                               Chitinase; insect; transgenic
biocide; insecticide; tobacco
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 SPTTPTTPSPTTTT---
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N-PSDB; AAT62557.
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                                                                                                                                                                                                                                                                    Manduca sexta
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                                                                                                                                                                                27-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                               Active-site
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183
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                                                                                                                                                                                                                                           457 TTPTTTPSPTT-----PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI
                                         KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL
                                                           KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                      RAAFIRVGKGWELIAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP
                                                                                                                                                                               LYKRPHD-QWAYEKLNVNDGLHIMBEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI
                                                                                                                                                                                                                     291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIOYDEYYNAPYGYNDKI
                                                                                                                                                                                                                                                                                                  450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE------VDGSEI
                                                                                                                                                                                                                                                                               349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS
                                                                                                                                                                                                                                                                                                                                           409 FECILGPSTTTPTPTTTTTTTT-----TTPTTPS-----PTTPTTPSPTTTPSP
                                                                                                                                                                                                                                                                                                                                                                       -----SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTAKPASTTKTTVKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imaginal disc growth factor; IDGF; chitinase related protein; CHRP;
tissue growth; wound healing; bone repair; cartilage repair;
angiogenesis; meat production; milk production; cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 KCYKEGD-IPHPINIHKYLVCEFVNGGWWVHIMPCPPGIIWCQEKLTC 552
                                                                                                                                                              LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED--
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Manduca sexta chitinase

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The present sequence is the protein sequence for the Manduca sexta gut chitinase. It was used to isolate the Drosophila melanogaster imaginal disc growth factor 4 (IDGF4) coding sequence. IDGF4 is a member of the chitinase related proteins (CHRP) and is involved in the promotion of expected to have mammalian homologues. The gene and protein are expected to have mammalian homologues. They can be used in the treatment of cancer, wound healing, tissue regeneration following arthritis, osteoporosis, other skeletal disorders and burns, for revitalising scartissue resulting from surgical procedures, irradiation, laceration, toxic chemicals, viral or bacterial infection or burns, to promote tissue growth during tissue engineering, for example tissues for skin graft replacements and bone responth, and to modulate the function of the female reproductive tract. In addition, they can also be used to increase meat, egg, sperm and milk production in animals. One possible method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKIHKHMS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPTTTPSPTT------PTP-TPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ATLATLAVLALATAV-----QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYGFAKIDBYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTIMISLGGWYEGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSKLKLGDPAKGMSPPGF1SGEEGVLSY1ELCQLFQKEE--WH1QYDEYYNAPYGYNDK1
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35.4%; Pred. No. 1.9e-52;
ive 79; Mismatches 210;
                    Disclosure, Col 53-58; 40pp; English
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Best Local Similarity 35.4°
Matches 208; Conservative
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Ä 554

ABP72619 standard; protein;

RESULT 15 ABP72619 (first entry)

11-JUN-2003

ABP72619;

EXXXE

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                                          Insecticide, pesticide, insect control, insect; toxin; chitinase; enzyme; neuropeptide; transgenic plant; crop protection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as a carrier to translocate toxic moiety inside plant pathogen, and a toxic
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                                                                                                                                                                                  /label= Mature_protein
85. .88
/note= "Asn is N-glycosylated"
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/note=__Asn is N-glycosylated"
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(ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
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/label= Signal_peptide
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/QEL 170	INAP 241 1: 7HSP 230	290 3TFI 289	JDKI 348 KGTQ 342	EKNS 408	PSP 456 : : :XTT 449	HLI 505 	
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KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDMEYPGAADRGGSFSDXDKFLYLVQEL	KDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP :	LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAMSIED :	RSKLKLGDBAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIOYDEYYNAPYGYNDKI 	WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 	FECILGESTITPTTTTTTTTTTTTTTTTPSP	TTPTTTPSPTTPTP-TTPTPAPTTSTPSPTTTBHTSBTPKYTTYVDGHLI 	KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC :
KYSHMVAQKSTRM	KDAFEPHGYLL 	LYKRPDETDELHT : LYKRPHD-QWAYE		WVGYDDLASISCK : WVGYEDPRSVEIK		TTPTTTPSPTT	
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Search completed: March 22, 2004, 06:51:46 Job time : 169.752 secs

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Sequence 632, 2 Sequence 1900,

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March 22, 2004, 06:59:34 ; Search time 113.53 Seconds (without alignments) 1265.926 Million cell updates/sec
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1 MKTIYAILSIMACIGIMNAS.....IMPCPPGTIWCQEKLTCIGE
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Sequence 45, Appl Sequence 270, App Sequence 278, Appl Sequence 278, Appl Sequence 278, Appl Sequence 17162, A Sequence 10644, A Sequence 19361, A Sequence 209667, Sequence 2399, Appl Sequence 11, Appl Sequence 11, Appl Sequence 1684, Appl Sequence 1684, Appl Sequence 1684, Appl Sequence 1684, Appl Sequence 1684, Appl Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Sequence 27319, Appl Sequence 2

5 US-10-369-493-6743
5 US-10-295-027-632
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ΩI	US-10-218-743-15	US-10-218-743-18	US-10-218-743-21	US-10-218-743-35	US-10-218-743-38	US-10-218-743-41	US-10-004-219B-10	US-10-161-547-2	US-10-004-219B-4	US-10-161-547-4	US-10-004-219B-9	US-10-161-547-14	US-10-161-547-15	US-10-004-219B-14	US-10-004-219B-1
	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
% Query Match Length DB	555	553	536	509	509	490	445	466	473	466	452	373	373	455	476
% Query Match	100.0	100.0	97.0	81.8	81.8	79.7	23.8	23.8	23.7	23.6	23.5	23.2	23.2	22.8	22.8
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ALIGNMENTS

Sequence 10415,

Sequence Sequence

RESULT 1

US-10-218-743-15

Squence 15, Application US/10218743

Publication No. US2030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McDer, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 2002-08-13
PRIOR PRILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-04-17
PRIOR PLING DATE: 1998-04-17
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PRIOR PLING DATE: 1998-04-17 Gaps ; 0 100.0%; Score 3107; DB 14; Length 555; 100.0%; Pred. No. 3e-220; Ative 0; Mismatches 0; Indels 0;) ORGANISM: Dermatophagoides farinae US-10-218-743-15 Query Match Best Local Similarity 100.C Matches 555; Conservative TYPE: PRT

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Sequence 18, Application US/10218743

Publication No. U220030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: HUNCER STILLS WA
APPLICANT: HUNCER STAIC R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-C-3
CURRENT APPLICATION NUMBER: US/10/218,743

CURRENT TILLING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PATENTIN UNMER: 00/096,565

PRIOR FILING DATE: 1998-04-17

SOFTWARE: PATENTING DATE: 1998-04-17
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                              CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                   EGSEKYSDWAANPTYRQQFIQSVLDFLQEYKPDGLDLDWEYPGSRLGNPKIDKQNYLALV
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LENGTH: 555
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APPLICANT: Hunter, Shirley Wu.
APPLICANT: Hunter, Shirley Wu.
APPLICANT: Hunter, Shirley Wu.
APPLICANT: Weber, Eric R.
ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROT
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FAPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 1999-04-15
FRIOR APPLICATION NUMBER: US/099,909
PRIOR FILING DATE: 1998-05-03
PRIOR FILING DATE: 1998-04-17
PRIOR PELLING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PALENTIN VOR: 2.0
SOFTWARE: PALENTIN VOR: 2.0
TRANSH NUMBER: DATE OF SEQ ID NOS: 49
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Sequence 35, Application US/10218743

Publication No. US20030096779A1

Sequence 35, Application No. US20030096779A1

APPLICANT: MocCall.
APPLICANT: MocCall.
APPLICANT: Whore DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USER THERROF

FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1990-40-13

PRIOR FILING DATE: 1990-40-15

PRIOR FILING DATE: 1990-0-12

PRIOR FILING DATE: 1990-0-13

PRIOR FILING DATE: 1990-0-13

PRIOR FILING DATE: 1990-0-13

PRIOR FILING DATE: 1990-0-17

PRIOR PRIOR DATE: 1990-0-17

PRIOR APPLICATION NUMBER: 60/098,565

PRIOR FILING DATE: 1990-0-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 35

LENGTH: 509
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Best Local Similarity 100.0%; Pred. No. 2e-213; Matches 536; Conservative 0; Mismatches 0; Indels
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Pred. No. 1e-178;
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                          435 ---PTTTDSTSETPKYTTYIDGHLIXCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491
                            9
                   61 CTHLMYGFAKIDEYKYTIQVFDPPQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                           121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV
                                                                                                                                                                                                                                                                                                                                  301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                                                                                                                                               361 KLAFLKELGVSGVMINSLENDDFKGRCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP
                                                                                                                        EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM
MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                                            CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY
                                                                                                                                                                                     RELIXDAFEPHGYLLTAAVSPGKDKI DRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNA
                                                                                                                                                                                                                                                  PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-38
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// ORGANISM: Dermatophagoides farinae
US-10-218-743-41
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| SEQUENCE 41.44-41
| SEQUENCE 41.44-41
| Publication No. US2030096779A1
| GENERAL INFORMATION:
| APPLICANT: McGall, Catherine A. |
| APPLICANT: McGall, Catherine A. |
| APPLICANT: Weber, Birley Wu APPLICANT: Weber, Bring W. |
| TITLE OF INVENTION: AND USES THEREOF |
| FILE REPERRNCE: AL-2-03 |
| CURRENT APPLICATION NUMBER: US/10/218,743 |
| CURRENT APPLICATION NUMBER: US/09/292,225 |
| PRIOR APPLICATION NUMBER: 60/098,909 |
| PRIOR PILING DATE: 1998-04-15 |
| PRIOR FILING DATE: 1998-04-15 |
| PRIOR FILING DATE: 1998-04-15 |
| PRIOR FILING DATE: 1998-04-15 |
| PRIOR FILING DATE: 1998-04-17 |
| PRIOR FILING DATE: 1998-04-17 |
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| PRIOR FILING DATE: 1998-04-17 |
| PRIOR FILING DATE: 1998-04-17 |
| SEQ ID NOS: 49 |
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                                                                                              1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFK
                                                                       1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
                                           Gaps
                                        52;
          Length 509;
                                          Indels
     2; DB 14;
1e-178;
ches 26;
        Query Match
Best Local Similarity 81.7%; Pred. No. 1e-1'
Matches 456; Conservative 24; Mismatches
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LENGTH: 490
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243 MHYYLNNGATRDKLVNGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 COLFOKBEWHIQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGVMIWSLEND 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFKGHCGPKYPLLNKVHMINGDEKNSYECLLGPSTTTPTPTPTTFTTTPT----- 415
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APPLICANT: Macrozyme
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: A mammalian mucinase, its recombinant diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: Which mucus is involved or infection diseases
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT APPLICATION NUMBER: 1001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                      63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122
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                                                                                                                                                                                                                                DPYQDDNHNSWEKRGYERFNYLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQ
                                                                                                                                                                 3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
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                                                                                                                    22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                           Gaps
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  Length 490;
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                                                        Indels
Query Match 79.7%; Score 2475; DB 14; Best Local Similarity 82.5%; Pred. No. 8.4e-174; Matches 443; Conservative 21; Mismatches 21;
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Pred. No. 5.3e-46;
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; Publication No. US20030087414A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%;
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Best Local Similarity
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173 SNRPRLMYTAAVAGGISNIQAGYEIPELSKYLDFIHVMTYDLHGSWEGYTGENSPLXKYP 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YILTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 DETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPP 306
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                     205 IDRAYDIKELNKLFDWMNWHYDYHGGWENFYGHNAPLYKRPDETDELHTYFNNNYTMHY 264
                                                                                                 265 YINNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                                                                                                                          325 FOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                          385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTTTPTTTFTTTTTTT 444
                                                                                                                                                                                                                                                                                                         ...----FSCNOG-----RYPLIQTURGELSLPYLPSGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10004219B
) Publication No. US20030087414A1
) GENERAL INFORMATION:
APPLICANT: Macrozyme
) APPLICANT: Aerts, Johannes M.F.G.
) TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: A mammalian mucinase, its recombinant diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases in TITLE OF INVENTION: which mucus is involved or infection diseases in TITLE OF INVENTION: Which mucus is involved or infection diseases in CURRENT APPLICATION NUMBER: US/10/004,219B
) CURRENT APPLICATION DATE: 2001-11-02
) NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LLNAQLGSAYN-----LICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 TYRQOFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 IMMASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGPAKIDEY
                                          191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: mouse AMCase; OTHER INFORMATION: amino acid sequence deduced from cDNA sequence US-10-004-219B-4
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23.7%; Score 736.5; DB 14; Length
Best Local Similarity 36.3%; Pred. No. 7.4e-46;
Matches 158; Conservative 72; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                   445 PSPTTPTTPSPTTPTTPSPTTPT 469
                                                                                                                                                                                                                                                                                                                                                                                            395 PELEVP-KPGOPSEPEHGPSPGODT 418
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ORGANISM: Artificial Sequence
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US-10-004-219B-4
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LENGTH: 473
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                                                                                                                                             FDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                 IDRAYDIKELNKIFDWMWWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFWWYTMHY 264
                                                                                                                                                                                                                                                                                                                  YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
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                                                                                                                        93 -EKRGYERFINILRIKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
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                                        RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
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Publication No. US20030143216A1

GENERAL INPORMATION:

APPLICANT: Gray, Patrick W.

TITLE OF INVENTION: CHITINABE CHITIN-BINDING FRAGMENTS

FILE REFERENCE: 27866/35407

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT PILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/267,574

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198

PRIOR PILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39
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                                                                            2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----
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Mismatches 150; Indels
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85;
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Best Local Similarity 34.24
Matches 152; Conservative
Conservative
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US-10-161-547-2
152;
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US-10-161-547-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 IDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| |:: :: |::|:| ||:|| || || CASTEVDKIA GANEDLYKROEESGAAAS-LNVDAAVQQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVMALDLDDFA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 -EKRGYERFNNIRLKNPELTIMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
292 GAYTRQAGFWAYYEICTFLRSGATEVW----DASQEVPYAYKANEWLGYDNIKSFSVKAQ 347
                                                                       -----LGISTE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLKELGVSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTT
                                                                                                                                                                                                                                                                                            APPLICANT: Gray, Partick W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVANTION: CHITINASE CHITIN-BINDING FRAGMENTS
FILE REFERENCE: 27566/33407
CURRENT APPLICATION NUMBER: US/10/161,547
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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                                                         348 WLKQNNFGGAMIWAIDLDDFTGSFCDQGKFPLTSTLNKA---
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Best Local Similarity 33.9%; Pred. No. 1.6e-45;
Matches 151; Conservative 85; Mismatches 151;
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US-10-161-547-4
i Sequence 4, Application US/10161547
i Publication No. US2003014321641
i GENERAL INPORMATION:
                                                                                                             419 TPTPTTTPTTTP 433
                                                                                                                                                393 GCTAPDVPSEPVTTP 407
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RESULT 11 US-10-004-219B-9

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                                                                                          APPLICANT: Macrozyme
APPLICANT: Macrozyme
APPLICANT: Macrozyme
APPLICANT: Marts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: which mucus is involved or infection diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
TITLE OF INVENTION: WHICH mucus is involved or infection diseases
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT APPLICATION NUMBER: US/10/004,219B
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNNEITT------IEWN
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Sequence 14, Application US/10161547

Sequence 14, Application US/10161547

Publication No. US20030143216A1

GARERAL INFORMATION:

APPLICANT: Gray, Patrick W.

APPLICANT: Gray, Patrick W.

TILLE OP INVENTION: CHILINASE CHITIN-BINDING FRAGMENTS

FILE REFERENCE: 27066/35407

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT APPLICATION NUMBER: US/09/267,574

PRIOR PILING DATE: 1999-03-12

PRIOR PILING DATE: BARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.5%; Score 729.5; DB 14; Length 37.0%; Pred. No. 2.3e-45; tive 69; Mismatches 144; Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: SITE

LOCATION: (1)..(452)

CTHER INFORMATION: /note="Mouse AMCase"
US-10-004-219B-9
   US/10004219B
Sequence 9, Application US/1000 Publication No. US20030087414A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.04
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
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us-09-662-293-18.rapb

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Sequence 14, Application US/10004219B

| Sequence 14, Application No. US2030087414A1
| Publication No. US2030087414A1
| GENERAL INFORMATION:
| APPLICANT: Macrozyme
| APPLICANT: Macrozyme
| APPLICANT: Boot, Rolf G.
| TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and TITLE OF INVENTION: Which mucus is involved or infection diseases in TITLE OF INVENTION: Which mucus is involved or infection diseases; CURRENT PILING DATE: 2010-11-02
| CURRENT APPLICATION NUMBER: US/10/004,219B
| CURRENT PILING DATE: 2011-11-02
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 2011-11-02
                                                                                                                                                                                                                                                                                                                                           289 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 345
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                                                                                              NDETLYQEFNGLKKAMPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 110
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                                                            FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 204
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CTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14
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ORGANISM: Homo sapiens
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APPLICANT: Tjoeker, Larry W.
TITLE OF INVENTION: CHITIMASE CHITIN-BINDING FRAGMENTS
FILE REFERENCE: 27866/35407
CURRENT APPLICATION NUMBER: US/10/161,547
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/267,574
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 39
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Publication No. US20030143216A1
GENERAL INFORMATION:
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      SOFTWARE: Patentin Ver. SEQ ID NO 14 LENGTH: 373 TYPE: PRI
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                                                                                                                              CRANISM: Homo sapiens
US-10-161-547-14
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RESULT 15
US-10-004-219B-1
Sequence 1, Application US/10004219B
Sequence 1, Application No. US2030087414A1
Sequence 1, Application No. US2030087414A1
GENERAL INFORMATION:
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in TITLE OF INVENTION: which mucus is involved or infection diseases in FILE REFERENCE: 2183-5136US
CURRENT APPLICATION UNMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 476
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                              288 FLKNGATQGWDAPQEVPYAYQGNVWVGYDNIKSFDIKAQWLKHNKFGGAMVWAIDLDDFT 347
325 FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
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                                                                                               385 G-HCGP-KNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTPTTPS 437
                                                                                                                             348 GTFCNQGKFPLI------STLKKALGLQSASCTAPAQPIEPITAAPSGS 390
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22.8%; Score 708.5; DB 14; Length 476;
Best Local Similarity 35.9%; Pred. No. 8.6e-44;
Matches 149; Conservative 75; Mismatches 154; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 22, 2004, 07:45:52 Job time : 114.53 secs
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ORGANISM: Artificial Sequence
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB_pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB_pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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DB	14	14	74	14	14	14	14	14	14	14	77	14	14	14	14
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& Query Match	100.0	100.0	100.0	82.1	82.1	82.1	24.5	24.5	24.3	24.2	24.2	23.9	23.9	23.5	23.5
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7005 6605	ESULT 1 15-10-218-743-21 Sequence 21, Applicate bublication No. UG200 BUNDICATION NO. UG200 BAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: MCA11, CAPPLICANT: APPLICANTON: TILE OF INVENTION: CURRENT FILING DATE: 1PRIOR PELICATION NUPRIOR PILING DATE: 1PRIOR PELICATION NUPRIOR PILING DATE: 1PRIOR PELICATION NUPRIOR PELICATION NUPRIOR PILING DATE: 1PRIOR PELICATION NUPRIOR PILING DATE: 1PRIOR PILING DATE: 1PRIOR PILING DATE: 1PRIOR PILING DATE: 1PRIOR PILING DATE: 1PRIOR FILING DATE	Match Local Simi es 536;
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) ORGANISM: Dermatophagoides farinae
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general information
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-25
CURRENT APPLICATION NUMBER: US/10/292,225
FRIOR PILING DATE: 1999-04-13
FRIOR PILING DATE: 1999-09-02
FRIOR APPLICATION NUMBER: 60/098,505
FRIOR APPLICATION NUMBER: 60/098,565
FRIOR PILING DATE: 1998-04-17
FRIOR APPLICATION NUMBER: 60/098,565
FRIOR APPLICATION NUMBER: 60/098,565
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FRIOR APPLICATION NUMBER: 60/082,013
FRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 15
FROM DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: D
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                              61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF
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Sequence 18, Application US/10218743

| Sequence 18, Application US/10218741
| Sequence 18, Application No. US20030096779A1
| CENERAL INFORMATION:
| APPLICANT: MCCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Hunter, Shirley Wu APPLICANT: WEBER, Eric R. TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEING DATE: 1998-13
| CURRENT PILING DATE: 2002-08-13
| PRIOR PILING DATE: 1998-09-02
| PRIOR PILING DATE: 1998-09-02
| PRIOR PILING DATE: 1998-09-03
| PRIOR PILING DATE: 1998-04-17
| PRIOR PILING DATE: 1998-04-17
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100.0%; Score 3014; DB 14; Length
Best Local Similarity 100.0%; Pred. No. 1.3e-212;
Matches 536; Conservative 0; Mismatches 0; Indels
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sequence 35, Application US/10218743

publication No. US203009677941

general information

publication No. US203009677941

general information

publication No. US203009677941

general information

perform medal, catherine A.

APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: AND USES THEREOF

FILE REPERENCE: AL-2-C3

CURRENT FILING DATE: 1090-04-15

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PRIOR PRIOR PRICE 1998-04-17

PRIOR APPLICATION NUMBER: 09/062,013

PRIOR APPLICATION NUMBER: 09/062,013

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PRIOR APPLICATION NUMBER: 00/062,013

PRIOR APPLICATION NUMBER: 00/062,013

PRIOR PRIOR PRIOR DATE: 1998-04-17

PRIOR APPLICATION NUMBER: 00/062,013

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Sequence 41, Application US/10218743

Publication No. US2030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: ADD USES THEREOF
FILE REFERENCE: AL-2-C3
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SOFTWARE: Patentin Ver. 2.0

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Best Local Similarity 82.5%; Pred. No. 3.6e-173;
Matches 443; Conservative 21; Mismatches 21;
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Sequence 10. Application US/10004219B

Publication No. US20030087414A1

GENERAL INFORMATION:

APPLICANT: Macrozyme

APPLICANT: Boot, Rolf G.

TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and

TITLE OF INVENTION: A mammalian mucinase, its recombinant diseases in

TITLE OF INVENTION: A mammalian mucinase, its recombinant diseases in

TITLE OF INVENTION: Which mucus is involved or infection diseases in

FILE REFERENCE: 2183-513-60S

CURRENT APPLICATION NUMBER: US/10/004,219B

CURRENT APPLICATION NUMBER: US/10/004,219B

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 10

LENGTH: 445

TYPE: PRT
                                                                                                                                                    262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 245
                                                                                                                                  MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 302
                                                                                                                                                                                                CQLFQKBEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 362
                                                                                                                                                                                                                                                                363 DFKGHCGPKNPLLNKVHNMINGDEKNSFBCILGPSTTTPTTFTTFTTFTTFTTFT 422
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123 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                      453 GHLIKCYKQGYLPHPTDVHKYLVCZYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 509
                                                                                                                                                                                                                                                                                                                                                                                                     483 GHLIKCYKEGDIPHPINIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 536
                                                                                  202 KDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT
                                                                                                                                                                                                                                                                                                                                                             142 SVLDPLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG
                                                                                                                                                                                                                     322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGVMIWSLEND
                                                                                                                                                                                                                                                                                   382 DFKGHCGFKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTPTTFTTTTTT-----
                                                               KDKIDRAYDIKELNKI PDWMVMTYDYHGGWENFYGHNAPLYKR PDETDELHTYFNVNYT
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FRATURE:
NAME/KEY: SITE
LOCATION: (1) .. (445)
OTHER INFORMATION: /note="Human chitotriosidase"
US-10-004-219B-10
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Best Local Similarity
Matches 152; Conserv
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                                                                                                                                                                                                                                                                                                 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLIGPSTTTPFTFFFFFFF-----434
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                                                                                                               261
                                                                                                                                             MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 302
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                                                                             KDKI DRAYDI KELNKI PDWMNYMTYDYHGGWENFYGHNAPLYKR PDETDELHTY FNVNYT
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82.1%; Score 2475; DB 14;
Best Local Similarity 82.5%; Pred. No. 3.8e-173;
Matches 443; Conservative 21; Mismatches 21;
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-38
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US-10-218-743-38
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426 PSPTTPTTTPSPTTPSPTTPT
                                            395 PELEVP-KPGQPSEPEHGPSPGQDT
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APPLICANT: Macrozyme; APPLICANT: Aerts, Johannes M.F.G.
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-004-219B-9
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170 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 228
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                                                 306 FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
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APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
FILE REFERENCE: 27866/35407
CURRENT APPLICATION NUMBER: US/10/161,547
PRIOR APPLICATION NUMBER: US/09/267,574
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: BALLIER APPLICATION NUMBER: 09/039,198
PRIOR FILING DATE: EALLIER FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NOS: 39
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                                                                                                                                                                                                                          426 PSPTTPTTTPSPTTPTTPSPTTPT 450
                                                                                                                                                                                                                                                         374 PELEVP-KPGQPSEPEHGPSPGQDT 397
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Similarity 34.2%;
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Matches 152;
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Best Local
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74 -EKRGYERFINILALKNPELTTMISLGGWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYK 132
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Sequence 4, Application US/10161547

Sequence 4, Application US/10161547

Publication No. US20030143216A1

GENERAL INFORMATION:

APPLICANT: Gray, Patrick W.

APPLICANT: Tjoelker, Larry W.

TITLE OF INTENTION: CHITINASE CHITIN-BINDING FRAGMENTS

FILE REPERENCE: 27866/3540

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT FILING DATE: 1999-06-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198

PRIOR PILING DATE: BARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 4.

FROM PATENTION OF: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 466;
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24.3%; Score 732; DB 14;
Best Local Similarity 33.9%; Pred. No. 2.3e-45;
Matches 151; Conservative 85; Mismatches 151;
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DGLDLDWEYPGSR-GSPPQDKHLFTVLVKEMREAFEQEAIESNRPRLMVTAAVAGGISNI 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boot, Rolf G.

TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
FILE REPERBNCE: 2183-51360S
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVTLYKAFNDLKNRNSKLKTLLAIGGWNFGTAPFTTMVSTSQNRQTFITSVIKFLRQYGF 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLF 306
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Publication No. US20030087414A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Macrosyme
APPLICANT: Macrosyme
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APPLICANT: Macrosyme
APPLICANT: Macrosyme
APPLICANT: Macrosyme
APPLICANTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
TITLE OF INVENTION: which mucus is involved or infection diseases
CURRENT APPLICATION NUMBER: US/10/004,219B
CURRENT FILING DATE: 201-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
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Pred, No. 3.4e-45;
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                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
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US-10-004-219B-4
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Best Local S
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:

O ID NO 4 LENGIH: 473

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                                                                                                                                                                                      16 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW-
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US-10-161-547-14

US-10-161-547-14

Sequence 14, Application US/10161547

PUDLICATION NO. US20030143216A1

GENERAL INFORMATION:

APPLICANT: Gray, Patrick W.

APPLICANT: Tjoelker, Larry W.

TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS

FILE REFERENCE: 27866/35407

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/267,574

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198

PRIOR APPLICATION STREET FRIENCE DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39
; OTHER INFORMATION: Description of Artificial Sequence: mouse AMCase; CTHER INFORMATION: amino acid sequence deduced from cDNA sequence US-10-004-219B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LGISTEGCTAPDVPSEPVTTP
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                                                                                                    Length
                                                                                                    24.2%; Score 729.5; DB 14; Length 37.0%; Pred. No. 3.6e-45; ive 69; Mismatches 144; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 FIGSFCDQGKFPLTSTLNKA----
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SEQ ID NO 14
                                                                                                         Query Match
Best Local Similarity 37.03
Matches 154; Conservative
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TYPE: PRT
ORGANISM: Homo Bapiens
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RESULT 14
US-10-004-219B-14

is Sequence 14, Application US/10004219B

sequence 14, Application US/10004219B

publication No. US20030087414A1

GENERAL INFORMATION:

APPLICANT: Macrozyme

APPLICANT: Macrozyme

TITLE OF INVENTION: is use in therapy or prophylaxis against diseases in TITLE OF INVENTION: is use in therapy or prophylaxis against diseases in TITLE OF INVENTION: which mucus is involved or infection diseases in TITLE REFERENCE: 2183-5136US

CURRENT APPLICATION NUMBER: US/10/004,219B

CURRENT PILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 -EKRGYERFINILKINPELITMISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLOEYK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in TITLE OF INVENTION: which mucus is involved or infection diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Score 708.5; DB 14; Length 35.9%; Pred. No. 1.2e-43; live 75; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(455)
; OTHER INFORMATION: /note="Human AMCase"
US-10-004-219B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/10004219B; Publication No. US20030087414A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
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23.5%
Best Local Similarity 35.9%
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
      346 G 346
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US-10-004-219B-1
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APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: CHITINABE CHITIN-BINDING FRACMENTS
FILE REFERENCE: 27866/31878.
CURRENT APPLICATION NUMBER: US/10/161,547
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/267,574
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: BALLIER APPLICATION NUMBER: 09/039,198
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10161547
Publication No. US20030143216A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-15
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US-10-161-547-15
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REFERENCE: 2183-5136US

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Query Match 23.5%; Score 708.5; DB 14; Length 476; Best Local Similarity 35.9%; Pred. No. 1.2e-43; Matches 149; Conservative 75; Mismatches 154; Indels 37; Gaps 10;
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                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human AMCase
CTHER INFORMATION: amino acid sequence deduced from cDNA sequence
US-10-004-219B-1
CURRENT APPLICATION NUMBER: US/10/004,219B CURRENT FILING DATE: 2001-11-02 NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 476
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Search completed: March 22, 2004, 07:45:53 Job time : 110.643 secs

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(without alignments)
929.256 Million cell updates/sec
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                                                                                                                      March 22, 2004, 06:30:23 ; Search time 162.975 Seconds
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    1586107 seqs, 282547505 residues

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                     Copyright
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                                                                                OM protein
                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                        Run on:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

genesequ1980s:* genesequ1990s:* genesequ2001s:* genesequ2001s:* genesequ2002s:* genesequ2003bs:* genesequ2003bs:* A Geneseq 29Jan04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Drosophil Prawn chi Drosophil Manduca s Manduca s HIMW-m Drosophil Bombyx mo Flea PCfC Flea chit Aedes aeg Chelonus Der HMW-m Der HMW-m Der HMW-m D. pteron D. pteron Anopheles Aay52525 House dus Flea Aau96328 | Aay52535 | Aau96339 | Aay52533 Aau96337 Aby72636 Abb72636 Abb72634 Aby71737 Aaw01824 Abb71737 Abp72619 1 Abb64366 Abp72625 Aae28197 Abp72635 Abp72633 CAbp72626 F Aay52523 Aau96327 Aae28199 Aae28203 SUMMARIES AAY52535 AAU96339 AAY52533 AAY52523 AAU96327 AAE28199 **AAU9632**8 **ABP72636** AAB07183 AAE28197 Query Match Length DB Score

Aaw08584 Human 50	Aaw40259 Human chi	Aay42425 MO-218 cl	Aae00432 Human chi	Aae25903 Human chi	Abb76291 Human chi	Adc24231 Human NOV	Aaw08585 Human 39	Adc24237 Human NOV	Aaw40260 Human chi	Aay42426 MO-13B cl	Aae00433 Human chi	Aae25904 Human chi	Abb76292 Human chi	Aaw31498 Human chi	Abr55544 Amino aci	Abr55543 Amino aci	Abu09914 Partial m	Adc51464 Chitotria	Abp72621 Human chi
AAW08584	AAW40259	AAY42425	AAE00432	AAE25903	ABB76291	ADC24231	AAW08585	ADC24237	AAW40260	AAY42426	AAE00433	AAE25904	ABB76292	AAW31498	ABR55544	ABR55543	ABU09914	ADC51464	ABP72621
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RESULT 1

Mite allergen protein; map; high molecular weight; HWW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation. House dust mite (D. farinae) mite allergen protein (map) PDerf98-536 AAY52525 standard, protein, 536 AA. Weber ER 98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524 N-PSDB; AAZ38579, AAZ38580. (first entry) Dermatophagoides farinae. Mccall CA, Hunter SW, WPI; 2000-052700/04 (HESK-) HESKA CORP. 22-FEB-2000 WO9954349-A2 16-APR-1999; 28-OCT-1999. 17-APR-1998; 02-SEP-1998; 13-MAY-1998 AAY52525; AAY5252

igh molecular weight Dermatophagoides nucleic acid polypeptides modify an animals' hypersensitivy to mite allergens. Novel high used to

Claim 3; Page 125-127; 154pp; English.

This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-556 (AAV52523). PDerf98-536 has a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HMM-map) composition. The HMM-map composition was allergen protein (HMM-map) composition. The HMM-map composition was faraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic

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compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
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brican house dust mite; antiallergic; mite; IgE; protein; immunoglobulin E; hypersensitivity;
                AAU96329 standard; protein; 536
                                                                                    HMW-map; American house
                                                                  Der HMW-map polypeptide #16
                                                  (first entry)
                                                                                                                     Dermatophagoides farinae,
                                                                                                    immunocomplex formation.
                                                                                            allergenic
                                                  15-JUL-2002
                                  AAU96329
                                                                                            mite
                                                                                    Der ]
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WO200222807-A2

21-MAR-2002

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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonprotein susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to a llergic response to a mite. The DNA and protein can be used in the allergic response that DNA map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus be reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96342 represent Der HWW-map protein on the invention
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                                                                                                                                                                                                                              mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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100.0%; Pred. No. 3.7e-210;
ive 0; Mismatches 0;
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14-SEP-2001; 2001WO-US028730.
                                           14-SEP-2000; 2000US-00662293
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Les 536; Conservative
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                                                                                                                                                                      2002-351888/38.
                                                                                      HESKA CORP
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SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ VFDPYQDDNHNSWEKRGYER FNNLRLKNPELTTMI SLGGWYEGSEKYSDMAANPTYRQQF

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240

200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259 YTWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300 379

439 480 499

536

VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 500 VDGHLIKCYKEGDIPHPINIHKYLVCEFVNGGWWYHIMPCPPGTIWCQEKLTCIGE

481

AAU96327 standard; protein; 555 AA

AAU96327;

ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

301

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361

320 ELCOLFOKEEWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE

260 YIMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI

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NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTFTTFTTPTTTPTTPTTPTTPTT

380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTFSPT TPTTTPSPTTPTTTPSPTTTTPSPTTPTPTPAPTTSTPSPSPTTTEHTSETPKYTTY 440 retrinsertresertresertreserterertresertresertrenesertreneserekyrry

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This sequence represents Dermatophagoides farinae mite allergen protein

(map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,

comportains 555 anino acids, and is a component of the Dermatophagoides

composition. The ENW-map composition was isolated from a D. farinae

homogenate by gel filtration, with each fraction being analysed for the

presence of proteins that bound to IgB present in mite-allergic dog

confosition. The allergenic proteins and peptides, and nucleic acids

encoding them, may be used in therapeutic compositions to modify an

antisera. Mite allergenic proteins and peptides, and nucleic acids

encoding them, may be used in therapeutic compositions to modify an

animal's hypersensitivity reaction to mite allergens. Animals that may be

treated include mammals and birds, especially felines, canines,

humans, other petes, and work or domestic animals. The proteins or

fragments may also be used to diagnose allergies via a skin test. The

proteins and peptides can also be used to raise antibodies, which have a

variety of potential uses. For example, they can be used as vaccines to

possively immunise animals against dust mite hypersensitivity, as

possively immunise animals against dust mite hypersensitivity, as

possively immunise animals against dust mite hypersensitivity, as

possively man perfect and as tools to recover desired dust mite
                                                                                                                                                                     Mite allergen protein; map; high molecular weight; HWW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                   House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-052700/04.
N-PSDB; AAZ38575, AAZ38576, AAZ38579, AAZ38578.
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/note= "Mature PDerf98-555"

    19 /note= "Signal peptide"

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                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                  Ä
                  AAY52523 standard; protein; 555
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98US-0085295P.
98US-0098909P.
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                                                                                                (first entry)
                                                                                                                                                                                                                                                                            Dermatophagoides farinae.
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13-MAY-1998;
02-SEP-1998;
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                                                       AAY52523;
                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                       Peptide
AAY52523
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New mite allergenic protein isolated from Dermatophagoides, designated
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                               Der HMW-map, American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 114-116; 161pp; English.
                                                                                                                                                                                                                                                         Weber ER;
                                                                                                                                                                                          14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                               14-SEP-2000; 2000US-00662293
                                                               Der HMW-map polypeptide #14.
                                          (first entry)
                                                                                                                           Dermatophagoides farinae.
                                                                                                                                                                                                                                                       Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                            WPI; 2002-351888/38.
N-PSDB; ABK69571.
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                                                                                                                                                WO200222807-A2.
                                         15-JUL-2002
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WO200222807-A2

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acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)s or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to 1gs, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention
designated Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 555 AA;
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                                                                                                SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ
                                                                SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGFAKIDBYKYTIO
                                                                                                                                                                 VPDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF
                                                                                                                                                                                                                                                                                                                                                                  YTWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEGVLSYI
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      Length 555;
                                       Indels
   Score 3014; DB 5;
Pred. No. 3.9e-210;
Mismatches 0;
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0
     100.0%;
Query Match
Best Local Similarity 100.
Matches 536; Conservative
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Der HMW-map, American house dust mite; antiallergic; mite; 1gE; mite allergenic protein; immunoglobulin E; hypersensitivity; AAU96328 standard; protein; 555 Der HMW-map polypeptide #15 (first entry) immunocomplex formation. 15-JUL-2002 AAU96328;

Dermatophagoides farinae.

The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the categories of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention n Dermatophagoides, designated for treating mite allergy. 1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGFAKIDEYKYTIQ 121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 200 PGKDKIDRAYDIKELNKIFDWANVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 80 VFDPYODDNHNSWEKRGYERFNNLRLKNPELITMISLGGWYEGSEKYSDMAANPTYROOF 181 PCKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN YTMHYYLNINGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 301 BLCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE Gaps ö Length 555; Indels Score 3014; DB 5; Pred. No. 3.9e-210; 0; Mismatches 0; New mite allergenic protein isolated from Der HMW-map protein, useful as a vaccine f Claim 12; Page 120-122; 161pp; English. Weber 100.0%; 100.0%; 14-SEP-2001; 2001WO-US028730 14-SEP-2000; 2000US-00662293 Query Match 100. Best Local Similarity 100. Matches 536; Conservative Hunter SW, WPI; 2002-351888/38 (HESK-) HESKA CORP N-PSDB; ABK69573 Sequence 555 AA; 21-MAR-2002 Mccall CA, 241 61 임 쉱 8 엄 ઠ 임 ठ g ठ ઠ

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240 259 300 360 379 480

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320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE NDDFXGHCGPKNPLLINKVHNMINGDEKNSFECILGPSTTTPTTTTTTTPTTTPSPT Ŋ

Page

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protein (map) Poerp98 490, the mature form of poerp98-509. Poerp98 490
thas a molecular weight of 98 kb, comprising 490 amino acids, and has a
high degree of homology with the D. farinae mature 98 kb allergen, mapp
(AAY52525). Nucleic acid molecules encoding Poerp98 490 were isolated
from a D. pteronyssius cDNA library by hybridisation with a probe
encoding the D. farinae high molecular weight map (HMW-map) composition.
Mite allergenic proteins and peptides, and nucleic acids encoding them,
may be used in therapeutic compositions to modify an animal's
hypersensitivity reaction to mite allergens. Animals that may be treated
include mammals and birds, especially felines, canines, equines, humans,
other pets, and work or domestic animals. The proteins or fragments may
peptides can also be used to caise antibodies, which have a variety of
potential uses. For example, they can be used as vaccines to passively
in munise animals against dust mite hypersensitivity, as positive controls
in test kits and as tools to recover desired dust mite allergens from a
mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
Wite allergen protein; map; high molecular weight; HWW-map; allergy; house dust miter; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fellne; canine; veterinary; antibody; vaccine; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents Dermatophagoides pteronyssius mite allergen
                                                    VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGMPVHIMPCPPGTIMCQEKLICIGE
                                  VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE
                                                                                                                                                                                                                                                                                 D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             115. .117
/note= "Asn is N-glycosylated"
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                                                                                                                                                       AAY52535 standard; protein; 490 AA.
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98US-0085295P.
98US-0098909P.
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(first entry)
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02-SEP-1998;
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22-FEB-2000
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AAY52535
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                                                                                                                                                                                                                                                183 KDKIDVAYELKELNQLFDMMVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242
                                                                                                                                          63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122
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                                                                                    3 KRDHNNYSKAPPARIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                DPYODDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE
                            52;
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mite allergenic protein; immunoglobulin E; hypersensitivity;
immunocomplex formation.
 Length 490;
                             Indels
; Score 2475; DB 3;
; Pred. No. 4.2e-171;
21; Mismatches 21;
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 82.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Der HMW-map polypeptide #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                             Matches 443; Conservative
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              Similarity
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Mite allergen protein, map, high molecular weight, HMW-map, allergy, house dust mite, IgE, immunoglobulin E, allergen, mapB, hypersensitivity reaction, therapy, treatment, diagnosis, human, feline,

canine; veterinary; antibody; vaccine; immunisation.

Location/Qualifiers

Peptide Protein

Dermatophagoides pteronyssinus.

/note= "Mature PDerp98-509" 'note= "Signal peptide"

20. .509

WO9954349-A2

28-OCT-1999

D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509.

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Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-troteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the catection of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunosomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96312. represent Der HWW-map pilnention
mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                              an isolated mite allergenic protein
                                                                                      Claim 12; Page 144-146; 161pp; English.
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DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQ 122 63 DPFQDDNHNSWEKHGYERFNNIRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362 DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTTPTTTTPTTFTTPT 422 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTTPTTTPTTTPTT---- 415 423 TITPSPITETITPSPITETITPSPITETTPTPAPTISTPSPITITEHISETPKYTIYUD 482 -----PTTTDSTSETPKYTTYID 433 536 3 KRDHNNYSKUPMRIUCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGFAKIDEYKYTIQVF SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG KDKI DRAYDI KELNKL FDWMVMTYDYHGGWENFYGHNAPLYKR PDETDELHTYFNVNYT 243 MHYYLNNGATRDKLVMGVPFYGRAMSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF Gaps GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 52; Length 490; 21; Indels 82.1%; Score 2475; DB 5; 82.5%; Pred. No. 4.2e-171; ive 21; Mismatches 21; Matches 443; Conservative Query Match Best Local Similarity Sequence 490 AA; m 63 363 123 183 183 243 303 303 363 416 483 q δ 셤 8 8 ద 8 8 ò 유성 ò a ò 셤 8 合

l high molecular weight Dermatophagoides nucleic acid polypeptides to modify an animals' hypersensitivy to mite allergens.

N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.

Novel high

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Weber ER

Accall CA, Hunter SW, WPI; 2000-052700/04

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62

(HESK-) HESKA

13-MAY-1998; 17-APR-1998;

98US-00062013. 98US-0085295P.

99WO-US008524

16-APR-1999;

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This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, comprising 509 amino acids, and has a high degree of homology with the D. farinae 98 kD allergen, mapB (AAX5253). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDNA library by PDerp98-509 were isolated from a D. pteronyssius cDNA library by map (MAW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to moleic acids encoding them, may be used in therapeutic compositions to moleic allergens. Animals confifty an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite the recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPYQDDNHNSWEKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ
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Best Local Similarity
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AAY52533 standard; protein; 509

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(revised)
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06-AUG-2003 22-FEB-2000

AAY52533;

RESULT 8
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWM-map protein, and its related nucleic acid. The Der HWM-map protein is useful for eliciting an immune response against Der HWM-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, act) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal the allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWM-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a disease. Antibodies that bind to Der HWM-map are useful for inhibiting
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                KDKI DVAYELKELNOLFDWMVWTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT
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KDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT
                                                               MHYYLNNGATRDKLVMGVPFYGRAWS1EDRSKLKLGDPAKGMSPPGF1SGEEGVLSY1EL
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Der HMW-map protein, useful as a vaccine for treating mite allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mite; IgE;
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N-PSDB; ABK69581.
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binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersenativity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention
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                                                                                                 Length 509;
                                                                                                                            Indels
                                                                                               82.1%; Score 2475; DB 5;
llarity 82.5%; Pred. No. 4.4e-171;
Conservative 21; Mismatches 21;
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                                                                       Sequence 509
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(first entry)

11-JUN-2003

ABP72636;

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Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response of against Der HWW-map protein or a reagent comprising a non-proteinaceus epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein cativity associated with a confirmance of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting confirming of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens formation, thus against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPFTFTTPSTTSTTTPT-----434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPYQDDNHNSWEKRGYERFNNLRLKNPELLTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTTTTPTTTPSPTTP 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 321
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                                                                                                                  mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAANSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHLIKCYKEGDIPHPINIHKYLVCEFV -- - NGGWWVHIMPCPPGTIWCQEKLTCIGE 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDKI DRAYD I KELNKL FDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTY FNVNYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIBDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
                                                                                                                                                                                                                  invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.1%; Score 2475; DB 5;
82.5%; Pred. No. 4.4e-171;
ive 21; Mismatches 21;
                                                                                                                                                                            Claim 12; Page 139-141; 161pp; English.
                    Weber ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 443; Conservative
                    SW,
                                                           WPI; 2002-351888/38
                    Hunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                             N-PSDB; ABK69583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 509 AA;
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ABP72636 standard; protein; 525 AA

RESULT 11 ABP72636 ID ABP72

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The present sequence is that of the mosquito Anopheles gambiae chitinase. This protein is used in claimed fusion proteins of the invention. Such this on proteins comprise a translocating moiety and a toxic moiety, where the translocating moiety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an insect-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable insect peptides and proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polymucleotides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease degradation in the insect gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 YQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSV 124
                                                                                                             pesticide; insect control; insect; toxin; chitinase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as a carrier to translocate toxic moiety inside plant pathogen, and a toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                      /note= "serine/threonine/proline-rich domain"
                                                                                                                                                                                                                                                                                                           /note= "possible trypsin activation site"
                                                                                                                           transgenic plant; crop protection; mosquito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.4%; Score 1007; DB 6; Length 5 39.5%; Pred. No. 1.5e-64; ive 86; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                       'note= "possible trypsin activation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYDU-) UNIV DURHAM.
(ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
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|abel= Signal_peptide
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                                                                                                                                                                                                                                                       label≈ Mature protein
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Fig 15; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2001; 2001GB-00019274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-2002; 2002WO-GB003598
                                                                            Anopheles gambiae chitinase
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                                                                                                                                                                                                                                                                                                                                                      401. .466
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                                                                                                                                                           Anopheles gambiae.
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                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                      WO2003014150-A2
                                                                                                                               neuropeptide;
                                                                                                             Insecticide;
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                                                                                                                                                                                                                                                                                                                                     Active-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                 LDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKD
                                                 SAGVSYDIPRISKSFHFINVMYYDMHGAMDSYCGINAPLYRGSADITDRLGQINVNASIH
                                                                                                                           YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ
                                                                                                                                          KLATEAWDLRWSEEQQVPYAVRNNQWVGYDDLRSVQLKVKYLLDQGLGGAMVWSLETDDF
                                                                                                                                                                                                                                  185 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                       305 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signalling; insecticide;
                                                                                                                                                                                                                                                                                                                            ---PCAGGRYGEVPHPTNCARYYICLTADTYYEFT-----CPPGTLF
                                                                                                                                                                                                                                                                                                             HLIKCY--KEGDIPHPTNIHKYLVC-----EFVNGGWWVHIMPCPPGTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                               protein;
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genes from Drosophila and
interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme;
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                       ----IEQGGYAKFTGLKTYNKQLKTMIAIGGWNEASSRFSPLVASNERRQQFIKNILKF
                                                                                                                                                                                                                                                                            LRONHFDGIDLDWEYPAHREGGKSRDRDNYAQFVQELRAEFEREAEKTGRTRLLLTMAVP
                                                                                                                                                                                                                                                                                                   PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTY---F
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                                                                                                                                                        15 RIVCYVGTWSVYH----KVDPYTIEDIDPFKCTHLMY---GFAKIDEYKYTIQVFDPYQD
                                                                                                                                                                                                       DNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDF
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                                                                                                                                     Gaps
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                                                                                                                                  107;
                                                                                                           Length 4498;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              control; insect; toxin; crop protection; prawn.
                                                                                                         28.2%; Score 848.5; DB 4; 34.9%; Pred. No. 7.3e-52; tive 81; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523
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(first entry)
                                                                                                                      Best Local Similarity 34.9
Matches 197; Conservative
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                                                                                    Sequence 4498 AA;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acid detection reagent for detecting 1000 or more
es from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 42003; 21pp + Sequence Listing; English
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                                                                 TTIGINPDPLDCTHYYLCSINTSGGFDEKEEVCPEGTLFNPQSFYC
                                         489 YKEGDIPHPINIHKYLVCEF-VNGGWWVHIMPCPPGTIWCQEKLTC
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35.2%; Pred. No. 3.4e-52;
cive 84; Mismatches 199;
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Matches 201, Conservative
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N-PSDB; ABL15840
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                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical.
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interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of prawn (Penaeus japonicus) chitinase. This protein can be used in claimed fusion proteins of the invention comprising a translocating moiety and a toxic moiety, where the translocating moiety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an arthropod-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable arthropod peptides and proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polynuclectides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease are also provided. The fusion protein is target-specific, and resists degradation in the insect gut. (Updated on 23-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 FDGLDMDWEYPTQRGGSPD-DYDNFAILMAELKQALQPEGMLLTAAVSAGKATIDPAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 PEISKSLDLINVMSYDLHGAWDDYTHHQSGLYAHPLDEGDNL--YLNVDFAISYWIEKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD--DNHNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 HIQYDEYYNAPYGY -- - NDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
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                                                                                                                                                                                                                                                                                                                      Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as carrier to translocate toxic moiety inside plant pathogen, and a toxi
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                                                                                                                                                                                            FOOD & RURAL AFFAIRS.
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                                                                                                                                                                                                                                      Edwards JP;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 14; 51pp; English.
                                                                                      06-AUG-2002; 2002WO-GB003598.
                                                                                                                             08-AUG-2001; 2001GB-00019274
                                                                                                                                                                                                                                      Fitches EC,
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KIDRAYDIKELNKLFDWMWMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH 244
                                                                                                                                                                                                                                                                                                                                                                                             PTTP----SPITPTT-----TPSPITPTTTPS--PTTPTTTPS--454
                                                                                                                                                                                                                                                                                                                                                                                                                                        PPNPDEGAVVAPTISTIKRPKPKPKPÍSSPLSPISAPGPVPIVGSSIPKPITKKPKKPKK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITITITIPAP --- EKSTEEPEEVVYPVDPVEPIDPEQPMGPQFDPNEIDCINRDFVPHP
                                                                                               245 YYLNNGATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYI
                                                                                                                                                                                            BLC-QLFQKEE-WHIQYDBYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWS
                                                                                                                                                                                                                                                                                         LENDDFKGHCGPKNPLLNKVH-NMINGDEKNSFECILGPSTTTPTFTTTP----TTPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s; insect; transgenic plant; biological control; baculovirus; insecticide; tobacco hookworm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manduca sexta larva epidermal and gut chitinase.
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/note= "proposed active site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Conserved_region-I
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/label= Sig_peptide
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/label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554
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useful for contro
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          An epidermal and gut chitinase (AAW01824) of Manduca sexta is encoded by cDNA clone 201 (AAT62557), isolated from a day-6 fifth instar whole larva cDNA library. The cDNA can be inserted into a vector for host expression of the chitinase protein, and may be utilised to control a population of insect pests. A recombinant baculovirus vector is provided for this purpose, as well as a transgenic tobacco plant that shows increased resistance to tobacco hornworm. Recombinant chitinase may also be expressed in host cells or larvae for subsequent purification and use as a biocide. The insect chitinase is expected to be more potent as an insect control agent than chitinases from other sources
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                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                    27.7%; Score 834; DB 2; Length 554; 35.9%; Pred. No. 5.7e-52; Indels ive 76; Mismatches 202; Indels
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                                                                                                                                                                                                                  Best Local Similarity
Matches 203; Conserv
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ALIGNMENTS

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Page Berner B.R., Hunter S., Stedman K., McCall C.;

Weber B.R., Hunter S., Stedman K., McCall C.;

"Cloning and Characterization of a 98 kDa Allergen from

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
98kDa HDM allergen.
Dermatophagoides farinae (House-dust mite).
Ekkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Astrogneiformes; Astrogneiformes; Astrogneiformes; Astrogneida; Psoroptidia; Analgoidea; Pyroglyphidae; Dermatophagoides.
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QBWR52
Q9GPG9
Q17411
Q26Q44
Q26Q44
Q26Q42
Q370D4
Q1723
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Best Local Similarity
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
NCBI_TaxID=182803;
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SMART; SM00636; Glyco_18; 1.
PROSTIE; PS01095; CHTTINASE_18; 1.
Glycosidaee; Hydrolase.
SEQUENCE 525 AA; 57211 MW; 3234360EEFF36165 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                  86; Mismatches 178;
                                                                                                                                  y Match 33.4%; Score 1007; DB 5; Local Similarity 39.5%; Pred. No. 5.2e-55; hes 210; Conservative 86; Mismatches 178:
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                  SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
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"Characterization of a novel gut-specific chitinase gene from the
"Characterization of a novel gut-specific chitinase gene from the
"Characterization of a novel gut-specific chitinase gene from the
"Thuman malaria vector Ampheles gambiae.";

J. biol. Chem. 272:28895-28900(1997).

BRBL; AF008575; AAB87764.1;

BRBL; AF008575; AAB87764.1;

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000576; C:extracellular; IEA.

GO; GO:000576; P:chitin binding; IEA.

RO; GO:0005075; P:chitin metabolism; IEA.

RO; GO:0005075; P:chitin metabolism; IEA.

RI nterPro; IRR001223; Glyco.hydro_18.

RI nterPro; IRR001223; Glyco.hydro_18.

RI nterPro; IRR001579; Glyco.hydro_18.

RI pfam; PF01607; GlW 14; 1.

R Pfam; PF00104; Glyco.hydro_18; 1.

R Probom; PD000471; Glyco.hydro_18; 1.

R Probom; PD000471; Glyco.hydro_18; 1.
                                                                                                                                                 VPDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165,
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MEDLINE=98030563; PubMed=9360958;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Score 869; DB 5; Length 1635; Pred. No. 8.5e-46; 95; Mismatches 196; Indels
                                  SMART; SM0656; Glyco 18; 3.
PROSITE; PS01095; CHITINASE_18; 3.
Hydrolase; Glycosidase; Chitin degradation; Glycoprotein;
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34.3%;
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(TrEMBLrel. 13, I
(TrEMBLrel. 25, I
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      SMART; SM00494; ChtBD2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 196; Conservative
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322
463
749
1338
                                                                                                    Hydrolase, Glycosid
Multigene family.
CARBOHYD 192
CARBOHYD 463
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                                                                                                                                                                                                                                              QVFDPYQDDNHNSWEXRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQ
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                                                                                                                                                                                                 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTI
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G0; G0:0005576; C:extracellular; IEA.

G0; G0:0005676; C:extracellular; IEA.

G0; G0:0008843; F:endochitinase activity, IEA.

G0; G0:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

G0; G0:0005975; P:carbohydrate metabolism; IEA.

G0; G0:0006012; P:chitin catabolism; IEA.

InterPro; IPR001257; Chitin bind PerA.

InterPro; IPR001257; Glyco hydro 18.

InterPro; IPR001579; Glyco hydro 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                          24;
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-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES
ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
HYDROLASES).
EMBL, AF026492; AAB81850.1; -.
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MEDLINE=98324849; PubMed=9662472;
MEDLINE=98324849; PubMed=9662472;
MEDLINE=98349; PubMed=9662472;
MCDLILINE=98349; PubMed=9840; PubMed=9840; Pubcosphila.";
                                                                 31.1%; Score 938; DB 5; Length 43 44.0%; Pred. No. 8.4e-51; ative 76; Mismatches 132; Indels
47238 MW; 929439397B9BC923 CRC64;
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Last annotation update)
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Pfam; PF00704; ClyCo hydro 18; 3.
ProDom; PD000471; Glyco hydro 18; 3.
                                                                                                                                   Conservative
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   431 AA;
                                                                                                    Similarity
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Best Local Simi
Matches 182;
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Q8MP05;
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                                                                                                                    Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Andlines W.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Andanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., RA Aburner M., Henderson S.N., RA Bardon R.C., Batter E.G., Helt G., Change M., Miklos G.L.G., Ratter E.G., Helt G., Change M., Miklos G.L.G., Ratter E.G., Helt G., Manpe M., Feefffer B.D., RA Besson K.Y. Bernos P.V., Barman B.P., Bhandari D., Bolshakov S., Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ratter M.R., Bouck J., Brokstein P., Brottier P., Burtis R.C., Busam D.A., Danlke C., Davenport L.B., Davies F., RA Berlos B., Delcher A., Danlke C., Ferraz C., Ferriera S., Fleischmann W., Rodoson K., Doup L.B., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P., Rodoson K., Doup L.B., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P., Roller C., Gabriellan A.E., Garg N. S., Gelbart W.M., Glasser K., Along F., Gorrell J.H., Gu Z., Gann P., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Inbegwan C., Julako P., Lei Y., Leviteky A.A., Li J., Li Z., Kanlison J.A., Katush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Merkulov G., Mishina N.V., Mobary C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Reinert K., Panlacton M., Stungki M., Shen H., Rayliams S.M., Woodanger T., Worley K., Sun B., Santh H., Wang Z.-Y., Wassarman D.A., Waller E., Wang A.H., Wang Z.-Y., Wassarman D.A., Waller E., Wang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Yang G., Shen H., Wang Z.-Y., Wassarman D.A., Wang Z.-Y., Wassarman D.A., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4498 AA; 493096 MW; AEE65CE0AAB25489 CRC64;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:000861; F:chitin binding; IEA.
GO; GO:0016798; F:hydrolase activity, acting or
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
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InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00494; ChtbD2; 1.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
                                                                       STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase
                                 FROM N.A.
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Reyer V., Freichard S., Bouhin H.;

Royer V., Freichard S., Bouhin H.;

Royer V., Freichard S., Bouhin H.;

Royer V., Freichard S., Bouhin H.;

Novel putative insect Chitinase with multiple catalytic domains:

Thormonal regulation during metamorphosis.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BR GO; GO:000576; C:extracellular; IEA.

GO; GO:000576; C:extracellular; IEA.

GO; GO:000843; F:endedhitinase activity, acting on glycosyl bonds; IEA.

GO; GO:0006576; C:extracellular; IEA.

GO; GO:0006579; F:endedhitinase activity, acting on glycosyl bonds; IEA.

GO; GO:0006579; F:endedhitinase activity, acting on glycosyl bonds; IEA.

GO; GO:0006579; F:endedhitinase activity.

GO; GO:0006579; F:endedhitin bind Pera.

Roy GO:0006579; P:enditin metabolism; IEA.

Roy GO:0006579; Glyco-hydro-189.

RiterPro; IRR001579; Glyco-hydro-189.

Rod Roy GO:000494; Glyco-hydro-189.

Rod Roy FDO:0041; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.

ROSITE; RS00165; Glyco-hydro-189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
LQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 FWAIDNDDFRGTCNGKPYPLIEAA-----KEAMVEALGIGINEVAKPSGPOKPSRSR 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 SRDNASNRNRLNGKTEAPLSSRRPSATRRPAVSSTQAPP--PSTTFKLTEAEGSSLYIGG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 -PSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHK 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GSDFKCEEEGFFQHPRDCKK 542
                                                                               161 LRONHFÖGIDLDWEYPAHREGGKSRÖRDNYAQFVOELRABFEREAEKTGRTRLLLTWAVP 220
                                                                                                                                                                                                                    221 AGIEYIDKGYDVPKLNKYLDWFNVLTYDFHSSHEPSVNHHAPLYSL--EEDSEYNYDAEL
                                                                                                                                                                   181 PGKDKIDRAYDIKELNKIFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTY---F
                                                                                                                                                                                                                                                                                                                                       238 NVNYTWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYIELCOLFOKE-EWH-IQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 VWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 T------TPSPTT---PTTTPSPTTPSPTTPSPTTPTT-----
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Tenebrionidae, Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 YLVCEFVNG----GWWVHIMPCPPG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Chitinase precursor (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 RASTIPPPPTIPDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Hydrolase; Glycosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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--KCAYDRFTALKQQNANLKALLAVGGWNEGSPKYSKYARADPALRNRFITSSIELLKKHG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 HIQYDEYYNAPYGY---NDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 WEKRGYERFINILALKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 IVCYVGTWSVYHK-VDPYTIBDIDPFKCTHLMYGRAKIDEYKYTIQVFDPYQD--DNHNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 RPGQIALGIPLYGRCWTLASQQETGYYAPAHQPGAAGDWTKSPGWLGYNEICYMQTTQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 KELNKLFDWMVWTYDYHCGWENFYGHNAPLYKRP-DETDELHTYFNVNYTMHYYLNNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 TRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTPTTTPSPTTPTTTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

[1]
HSSP; P07254; ICTN.

GO; GO:000861; F:chitin binding; IEA.

GO; GO:000861; F:chitin binding; IEA.

GO; GO:000861; F:chitin binding; IEA.

GO; GO:0008075; F:chitin metabolism; IEA.

GO; GO:0006375; P:chitin metabolism; IEA.

GO; GO:000630; P:chitin metabolism; IEA.

InterPro; IPR001223; Glyco hydro 18.

InterPro; IRR01579; Glyco hydro 18.

PEam; PP0704; Glyco hydro 18; 1.

ProDom; PD000471; Glyco hydro 18; 1.

ProDom; P0000471; Glyco hydro 18; 1.

ProDom; P0000471; Glyco hydro 18; 1.

SMART; SM00636; Glyco hydro 18; 1.

PROSITE; PS001955; CHITINASE 18; 1.

SRQUENCE 467 AA; 51765 NW; 499P7095774CA445 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%; Score 837.5; DB 5 34.8%; Pred. No. 1.8e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2448 AAPVGGIDVTEGAYKVVCYFINM--AMYRQGD-----GKYLPQDIDASLCTHINYGFA 2498
                                                                                                                                                                                                                                                                                                                                                                                                              126
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                                                                                                                                                                                                                                                                     NP - - - MRIVCYVGTWSVYHK - VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 GKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICTNVINKGWTVVRDRRGRIGPYAHLRDQWVSFDDIGMIRHKSEFIRAMGLGGGMIWALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 NDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPT-PTTTPT-TPTTTPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2328 KPTPKPSTPPYEPQKPSTQKPSYGTTESPEPVMPPDSVPCRGRLFVADEKNCNQYYLCNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2388 GELQLQVCPNGLFWNRDHCDWPENTECHPDGTTTAAPSTTTQTLEVEVPEVPEVPEPVTTP
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TITPSPTTPTTPTPAPTTSTPSPTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYL------VCEFVNGGWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe T., Kono M., Aida K., Nagasawa H.; 
"Purification and molecular cloning of a chitinase expressed in the hepatopancreas of the penaeid prawn Penaeus japonicus."; 
Blochim. Blophys. Acta 0.0-0(1997).
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Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Bumalacostraca, Bucarida, Decapoda, Dendrobranchiata, Penaeoidea,
                                                                                                                                      Query Match 27.9%; Score 842; DB 5; Length 2838; Best Local Similarity 32.2%; Pred. No. 8e-44; Aatches 198; Conservative 92; Mismatches 205; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TPSPTTPTTP-SPTT----PTTTPSPTTP-----
      1 20 POTENTIAL.
21 2838 CHITINASE.
2838 AA; 321407 MW; 608B3F2A8E98B9B7 CRC64;
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01-JAN-1998 (TrEMBLrel, 05, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467
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                                     CHAIN
SEQUENCE
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RY STUDINGE KNOWN N.

RY STRAIN=Berkelen's

RX MEDLINES-21950006 Pubmed=10731132;

RADIO CALL

RADIO COLLINIER S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADIO CALL

RADIO CG., Mortman J.E., I. P.W., Hoskins R.A., Galle R.F.,

RADIO G.G., Mortman J.E., Yandell M.D., Zhang Q., Chen L.X.,

RADIO G.G., Mortman J.E., Yandell M.D., Zhang Q., Chen L.X.,

RADIO CG., Mortman J.E., Yandell M.D., Radrows-Pfannkooh C., Batiwin D.,

RADIO C., Barder E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RADIO S. M., Barden M., Baxendal J., Bayraktaradylu L., Beasley E.M.,

RADIO BOTCHAN M., Bennan B.P., Bhandari D., Bolshakov S.,

RADIO BOTCHAN M., Bennan B.P., Bhandari D., Dolats S.M.,

RADIO S., Dolaten D.A., Dony D.E., Downes M., Dietz S.M.,

RADIO S., Dolater A., Dony E. C., Davenport L.S., Davise S.M.,

RADIO S., Dolater A., Dony E. C., Davenport L.S., Davise S.M.,

RADIO S., Dolatel A., Dony C., Berrar C., Perriac S., Dunkov B.C., Dunn P.,

RADIO S., Dolatellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RADIO S., Dolatellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RADIO S., Dolatellan A.E., Garg N.S., Kulp D., Harrish M.,

RADIO S., Mortell S., Molnicoh T.G., Molan P., Harrish M.,

RADIO S., Mattei B. Molnicoh T.G., Molan P., Harrish M.,

RADIO S., Mattei B. Molnicoh T.G., Molan P., Morberton D.,

RADIO S., Mattei B. Molnicoh T.G., Moland J., Di. Z., Liang Y., Lin X.,

RADIO S., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L,

RADIO D.R., Nelson K.A., Noberry C., Morris J., Pull Y., Shen H.,

RADIO D.R., Radrowskiamos I.S., Pollard J., Pull Y.,

RADIO D.R., Nelson K., Sunders R.D., Strong R., Santh H.,

RADIO D.R., Nelson K., Sunders R., Verlee R., Shen H.,

RADIO S., Sidan-Kiamos I., Simpson M., Strong R., Santh H.,

RADIO S.M., Wassarman D.A., Weinstender R., Verlee R., Wang A.L., Wang X.,

RADIO S.M., Walley R., Religetton M., Strong R., Santh H.,

RADIO S.M., Walley R., Sauders R., Religetton M., Shugesten D.,

RADIO S.M., Walley R., Religetton M., Strong R., Santh H.,

RADIO S.M., Walley R., Religetton M., Stro
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S. STRAIN=BERKELEY;
S. STRAIN=BERKELEY;
S. STRAIN=BERKELEY;
S. STRAIN=BERKELEY;
S. STRAIN=BERKELEY;
S. STRAIN=BERKELEY;
S. GONZALEZ M., Charlez C., Dorsett V., Farfan D., Frise E., George R., R. Gonzalez M., Calain, P. Lib P., Liao G., Miranda A., Mungall C.J.,
R. Munco J., Pacleb J., Parages V., Park S., Phouanenavong S., Wan K.,
R. Nunco J., Pacleb J., Parages V., Park S., Phouanenavong S., Wan K.,
S. Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
B. BMBL; AR003701; AAL29101.1; -
DR RDL; AX061553; AAL29101.1; -
DR GO; GO:0005576; C: Catracellular; IEA.
DR GO; GO:000501; F: chitin binding; IEA.
DR GO; GO:0005030; P: chitin binding; IEA.
DR GO; GO:0005030; P: chitin metabolism; IEA.
DR GO; GO:0005030; P: chitin bind Pera.
DR HIGEPRO; IPR001223; Glyco-Inducells.
DR InterPro; IPR001223; Glyco-Inducells.
DR InterPro; IPR001239; Glyco-Inducells.
DR Probom; PR000411; Glyco-Inducells.
DR Probom; PR000411; Glyco-Inducells.
DR Probom; PR000411; Glyco-Inducells.
DR Probom; PR0010411; Glyco-Inducells.
DR Probom; PR0010411; Glyco-Inducells.
DR Probom; PR0010411; Glyco-Inducells.
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35.2%; Pred. No. 2.4e-44;
ive 84; Mismatches 199;
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SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
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Best Local Similarity
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S_{\mathcal{A}}
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22;

Gaps

87;

Indels

Conservative

Matches 201;

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NHNSWEKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFL 128
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SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 TITITITIPAP---EKSTEEPEEVVYPVDPVEPTDPEQPMGPQFDPNEIDCTNRDFVPHP
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B. Submitted (OCT-2000) to the PENBL/GenBank/DDBJ databases.

R. RML; AF315689; AAN74647.1 - ...

R. GO; GO:0005576; C:extracellular; IEA.

R. GO; GO:0006576; C:extracellular; IEA.

R. GO; GO:0006787; F:hydrolase activity; IEA.

R. GO; GO:0016787; F:hydrolase activity; IEA.

R. GO; GO:0016787; F:hydrolase activity; IEA.

R. GO; GO:001575; P:carbohydrate metabolism; IEA.

R. GO; GO:000575; P:carbohydrate metabolism; IEA.

R. InterPro; IPR001223; Glyco_Hydro_18.

R. InterPro; IPR001223; Glyco_Hydro_18.

R. InterPro; IPR00123; Glyco_Hydro_18AS.
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Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Litopenaeus.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ProDom; PD000471; Glyco hydro 18; 1.
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Pfam; PF00704; Glyco hv
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RA Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dother C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Hauvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kaft C., Kravitz S., Kull D., Lai Z.,
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R. Lakko P., Lai Y., Leviteky A.A., Li J., Liang Y., Lin X.,
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RA Merkulov G., Milshina N.V., Mobarry C., Moris J., Moshrefi A.,
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RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weiseenbach J.,
RA Jeng K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhan X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
REGIOS R.A., Myers E.W., Rubin G.M., Venter J.C.;
REGIOS R. RESIS POTZEA; JCTN.
RESIS, POTZEA; JCTN.
RESIS, POTZEA; JCTN.
RESIS, POTZEA; JCTN.
RESIS, POTZEA; JCTN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKN - - - VVCYQGTWSVYRPGLGKFGMEDIDPFLCTHLIYAFLGIEE - TGQLRVIDAYLDL
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GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 000561; F: chitin binding; IEA.
GO; GO: 0005975; P: carbohydrate metabolism; IEA.
GO; GO: 0006457; P: protein folding; IEA.
GO; GO: 0006457; P: protein folding; IEA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR001253; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
Ffam; PF01607; CEM 14; 1.
Pfam; PF01607; CEM 14; 1.
Pfam; PF01607; CEM 14; 1.
Pfam; PF01607; CAM 14; 1.
ProDom; PD000471; Glyco hydro 18; 1.
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PROSITE; PS00453; FKBP_PPIASE_1; 1.
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SMART; SM00636; Glyco_1
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                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                    116
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                                                                                                                                                                                                                                                                                                                   WEKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYROOFIOSVLDFLOEYK 132
                                                                                                                                                                                                                                                                                                                                                                                                                FDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDI 192
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                                                                                                                                                                                                                      16 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD--DNHNS
                                                                                                                                                                                                                                                 1 NVCYPGSWAAYRQGLGKFDVEDIDPKICTHIIFGFAGL-AHDSSIRVLDPWNELCDNYG-
                                                                                                                                                                                                                                                                                                                                           117 FDGLDMDWEYPTORGGSPD-DYDNFVILMAELNQALHAEGMLLTAAVSAGKATIDPAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELNKL FDWMVWTYDYHGGWENFYGHNAPLYKRP-DETDELHTYFNVNYTMHYYLNNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 RPGQIALGIPLYGRCWILASQQEIGYYAPAHQPGAAGDWIRSPGMLGYNEICYWRITTQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 HIQYDEYYNAPYGY---NDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 TVVDDPAMNEPYTYYFPMNNIWCSYDHAASVAIKAEYAKSKGLAGTMVWSVETDDFRGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTTTTPTTTPTTTPTTTPTTTPSP
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                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

NCBI_TaxID=7227;
                                                                                                                            Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 H-----NRKYHLI----KTMVEVFGGGSITEP-----
                                                                                                                                                                          Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQPGLNPDPLDCTHYYLCSLNTSGGYNEKEEVCPEGTLYNPQSYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKEGDIPHPINIHKYLVÇEF-VNGGWWVHIMPCPPGTIWCQEKLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------pplptitrdpneptitirapp----pg-----
                                                                              734A830C6F47F4CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                       Score 831.5; DB 5;
Fred. No. 4.2e-44;
87; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
    SMART; SM00494; ChtBD2; 1.
PROSTT; SM00636; GlyCo_18; 1.
PROSTTE; PSU01095; CHTTINABE 18; 1.
SEQUENCE. 467 AA; S1958 NW; 734
                                                                                                                          27.6%;
34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25, CG9357 protein.
                                                                                                                  Query Match 27.6%
Best Local Similarity 34.2%
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09W2M7
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  141 DGLDLDWEYPGAADRGGSFSDKDEFLYFVQELKRAFIRADRGWELTAAVPLANFRLMEGY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL; AJ345054; CAC87888.1; -.

REMEL; AJ345054; CAC87888.1; -.

REMEL; AJ345054; C:extracellular; IEA.

GO; GO:0008061; F:chtin binding; IEA.

GO; GO:0016798; F:hydrolase activity; IEA.

RO; GO:0016491; F:oxidoreductase activity; IEA.

RO; GO:0016491; F:oxidoreductase activity; IEA.

RO; GO:0016491; F:hydrolase activity; IEA.

RO; GO:0016491; F:hydrolase activity; IEA.

RO; GO:0016491; F:oxidoreductase activity; IEA.

RO; GO:001690; F:hydrolase activity; IEA.

RO; GO:001691; F:oxidoreductase activity; IEA.

RO; GO:001691; F:oxidoreductase activity; IEA.

RO; GO:001691; F:oxidoreductase activity; IEA.

RICEPPO: IPRO01223; Glyco_Hydro_18.

RICEPPO: IPRO01879; Glyco_Hydro_18.1.

RODGON; PEODON; PEODON; ALDENYDE DEHYDR CYS; 1.

RARRT; SMO0494; CHED2; 1.

REMART; SMO0494; CHED2; 1.

REMART; SMO0494; CHED2; 1.

REMART; SMO0495; CHITINASE_18; 1.

REMART; ROSTIE; PSO1095; CHITINASE_18; 1.

REMART; ROSTIE; PSO1095; CHITINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.

REMART; RICEPPORTIANE SETAINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bufo japonicus (Japanese toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Bufonidae, Bufo.
NCBI_TaxID=8387,
                                                                                                                                                                                                                                                                                                              ::: ||||| || :||| || :|| || 373 AIDMDDFKGLCGEENPLIKLIH-----KHMSTYTVPPARTGHATPTPEW--ARPPSTP
                                           191 DIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTWHYYLNNG
                                                                  201 HVPELCQELDAIHVMSYDLRGNWAGFADVHSPLYKRPHD-QWAYEKLNVNDGLNLWEEKG
                                                                                                                          251 ATRDKLVMGVPFYGRAWSIED------RSKLKLGDDAKGMSPPGFISGEEGVLSY
                                                                                                                                                                 .-----WAY
                                                                                                                                                                                                        300 IELCOLFOKE -- EWHIOYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVW
                                                                                                                                                                                                                                              313 YEICTEVDADGSGWTKKWDEFGKCPYAYKGTOWVGYEDPRSVEIKMNMIKEKGYLGAMTW
                                                                                                                                                                                                                                                                                                                                                                    415 TIPSPITPITIPSPITIPITIPSPITIPITIPSPITPIPIPIPAPITISTPSPITITEHISET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thesis (2001), Department of Department of Biology, Waseda University,
                                                                                                                                                                                                                                                                                     SLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTT---TPTPTTTPTTTP
                                                                                                                                                                                                                                                                                                                                                                                                             424 SDPSEGDPI----PTTTTTTVKPTTTRTTARPT--TTTTKVPHGTTEEDFDINVRPEVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 PKYTTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 PPIENEVDNADV-CNSEDDYVPDKKECSKYWRC--VNGEGVQ--FSCQPGTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 488;
                                                                                                                                                 260 CPINKL/VVGIPFYGRSFTLSAGNNNYGLGTYINKEAGGGDPAPYTNATGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.3%; Score 823; DB 13; Length 4 Best Local Similarity 34.7%; Pred. No. 1.5e-43; Matches 186; Conservative 88; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOAD PANCREATIC CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54319 MW; E75E1AD3CB2B4919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foad pancreatic chitinase (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tokyo, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oshima H.;
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                                                                                                                                                                                                                                                                                       358
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Q90W34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGLDLDWEYPGSR-LGNPKIDKONYLALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAY 190
306 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 365
                                                                                                                                            GHCGPK-NPLLNKVHNMINGDEKNSFECILGPSTITPTTTTTTTTTTTPTTTPTT 424
                                                                                                                                                                                                                             425 TPSPTTPTTTPSPTTPTTPSPTTPTPTPTPTPAPTTSTPSPTTTEHTSETPK--YTTYVD 482
                                                                                                                                                                                                                                                                     411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVCYFSNWAVYRPGVGRYGIEDIPVDLCTHLIYSFIGVTEXSSEVLIIDPELD----V 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                     388 ----NTPSGLTTESNRESPSEGFSCPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                 412 A-----PAGYIRDPDNCSKFYYC----SGGKTHNFDCPSGLNFDLDTKSC 452
                                                                                                                                                                                                                                                                                                            483 GHLIKCYKEGDIPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 826; DB 5; Length 544 37.3%; Pred. No. 1.1e-43; tive 71; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 AA; 61069 MW; 89872DFC1DA23753 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                  367 GTCGQOPYPLLHEINRVLFGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bombyx mori (Silk moth)
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PS01095; CHITINASE 18; 1.
557 AA; 62227 MW; 2CF7827D6A294AD5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bombyx mori (Silk moth)
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
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                                                         NDDVLYKQFNDLKQKNKNLVTLLAIGGWNFGTQKFTDMVASSGNRSIFIKSVIAYLRQNN
                                                                                                                                                                                                                                                     FDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDK
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                         RIVCYVGTWSVYH-KVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                               186 IDRAYDIKELNKLPDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Tortricinae, Choristoneura.
NCBI_TAXID=7141;
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Zheng Y., Zheng Y., Cheng X., Ladd T., Krell P.J., Arif
Retnakaran A., Feng O.;
"A molt-associated chitinase CDNA from the spruce budwor
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
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SEQUENCE FROM N.A.
STRAIN=Kinshu x. Showa; TISSUE=Integument;
STRAIN=Kinshu x. Showa; TISSUE=Integument;
STRAIN=Kinshu b.M., Koga D.;
"Molecular banat B.M., Koga D.;
"Molecular cloning of Bombyx mori chitinase cDNA: a unique insert '
"Molecular cloning of Bombyx mori chitinase cDNA: a unique insert '
"Molecular cloning of Bombyx mori chitinase cDNA: a unique insert '
"Molecular mass of the encoded base pairs reduced the apparent molecular mass of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded companies of the encoded co
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO52914; BAB20017.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
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Last annotation update)
Query Match 27.3%; Score 821.5; DB 5; Best Local Similarity 34.7%; Pred. No. 2.2e-43; Matches 193; Conservative 79; Mismatches 207;
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Bombyx mori:

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SEQUENCE FROM N.A.

STRAIN=Kinshu X Showa hybrid; TISSUE=Integument;

XX MEDINE=21124800; PubMed=1122960;

Abdel-Banat B.M.A., NENGal D.;

"A genomic clone for a chitinase gene from the silkworm, Bombyx mori:

In sect Biochem. Mol. Biol. 31:497-508(2001).

Insect Biochem. Mol. Biol. 31:497-508(2001).

EMBL; AB048355; BAB13481.1;

CO; GO:0008061; Fichtin binding; IEA.

RO; GO:0008061; Fichtin binding; IEA.

RO; GO:0008943; Fichdcohitinase activity, acting on glycosyl bonds; IEA.

RO; GO:0008943; Fichdcohitinase activity, acting on glycosyl bonds; IEA.

RO; GO:0008979; Pichtin metabolism; IEA.

RO; GO:0008979; Pichtin metabolism; IEA.

RINE-FPO; IPR001223; Glyco-hydro-18.

InterPro; IPR001259; Glyco-hydro-1845.

Pfam; PF01607; CBM 14; 1.

Probom; PP01607; CBM 14; 1.

Probom; PP01607; CBM 14; 1.

Probom; PP01607; CBM 14; 1.

Probom; PP01607; CBM 14; 1.

PR Probom; PP01607; CBM 14; 1.

PR Probom; PP01607; CBM 14; 1.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00494; ChtBb2; 1.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
Glycosidase; Hydrolase; Signal.
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                                        on glycosyl bonds;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            C36C71E3B84DF8F8 CRC64;
     GO, GO:0008843; F:endochitinase activity, IEA.
GO; GO:0016798; F:hydrolase activity, acting on glo GO:0016798; F:hydrolase activity, acting on glo GO:0016798; F:hydrolase activity, acting on glo GO:0016375; F:carbohydrate metabolism; IEA.
GO; GO:0016376; P:chitin metabolism; IEA.
InterPro; IPR001525; Chitin bind PerA.
InterPro; IPR001523; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Fam; PF01607; CBM 14; 1.
Fram; PF01607; CBM 14; 1.
Fram; PF01607; Glyco_hydro_18; 1.
Frobom; PD00041; Glyco_hydro_18; 1.
FROSITE; PS01095; CHITINASE_18; 1.
Glycogldase; Hydrolase; Signal.
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CHITINASE.
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POTENTIAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 SDSRARIVCYFSNWAVYRPGVGRYGIEDIPVDLCTHLIYSFIGVTEKSSEVLIIDPELD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 NHNSWEXRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                  Length 543;
                                                                                                                                                      27.2%; Score 819; DB 5; Length 54 36.6%; Pred. No. 3e-43; Live 72; Mismatches 203; Indels
                                        543 AA; 60982 MW; DE29675D83AEC2EF CRC64;
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                                                                                                                                                 Query Match
Best Local Similarity
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chitinase precursor (EC 3.2.1.14)

CHI. Bombyx mori (Silk moth)

543 AA

PRELIMINARY;

Q9GV05, Q9GV05;

RESULT 15 099705 1D 09970 AC 09670 DT 01-MA DT 01-MA DT 01-MA DT Chiti GN CHI.

. Mon Mar 22 11:57:36 2004

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g

520 CPPGTIW 526 | ||||: 518 CQPGTIF 524

Search completed: March 22, 2004, 06:59:27 Job time : 108.855 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 22, 2004, 06:31:13 ; Search time 20.5581 Seconds (without alignments) 1357.597 Million cell updates/sec Run on:

US-09-662-293-21 3014 1 SIREDHNDYSKNPMRIVCYV......IMPCPPGTIWCQEKLICIGE 536

Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	mandu	Q13231 homo sapien	mus m	drosc		caen	SUB E	ovis	BUM	-	Q60557 mesocricetu	Q28042 bos taurus	рошо	рошо	papic	Q15782 homo sapien	Q9d7q1 mus musculu	P29030 brugia mala	Q9w5u2 drosophila	P20533 bacillus ci	-				O10363 orgyia pseu	autogra	P11797 serratia ma	P36909 streptomyce		strept	9519	275 therm	2817
SUPPREKIES	ΙD	CHIT MANSE	CHII HUMAN	CHIA MOUSE	CHI1_DROME	CHIA HUMAN	CHIT CAEEL	OGP PIG	OGP_SHEEP	C3L1_MOUSE	OGP_MOUSE	OGP_MESAU	OGP_BOVIN	OGP_HUMAN	C3L1 HUMAN	OGP PAPAN	C3L2_HUMAN	CHT1_MOUSE	CHIT_BRUMA	CHI3_DROME	CHI1_BACCI	CHI1_APHAL	CHIA_SERMA	CHI4_TRIHA	CHIA_ALTSO	CHIT_NPVOP	CHIT_NPVAC	CHIB SERMA		CHI1_COCPO		CHID VIBFU	VTP3_TTV1V	MUC2_HUMAN
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	Score	834	738	727.5	723	708.5	705.5	694.5	682.5	680	680	677.5	673	667.5	660	654	630	611.5	604.5	576	561	409.5	407.5	402.5	384	377.5	360.5	353	341	339.5	326	280	266.5	259
	Result No.	H	7	m	4	'n	v	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q62635 rattus norv Q05049 xenopus lae O1041 orgyia pseu P10667 xenopus lae P22533 caldocellum P44918 zea mays (m Q06885 dictyosteli P47179 saccharomyc P22659 dictyosteli P09805 kluyveromyc P24152 sorghum bic P02840 drosophila
MUCZ_RAT MUCI_XENLA Y091_NPVOP MUAI_XENLA MANB_CALSA EXTN_MAIZE EXTN_MAIZE GP10_DICDI DAN4_YEAST GTN6_DICDI KUN6_DICDI KUN6_DICDI KUN6_DICDI KUN6_DICDI KUN6_DICDI
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1513 6623 2769 13311 1341 11611 1161 1166 1166 1166 11
88777777776 61190000000111199
244 238 238 223 223 221 221 221 221 221 221 23 208 208 204
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ALIGNMENTS

RESULT 1 CHIT MANSE ID CHIT MANSE STANDARD; PRT; 554 AA. AC P34362.			-0201441	-!- CATALYTIC AC acetyl-D-glu- -!- SUBCELLULAR -!- TISSUE SPECI -!- DEVELOPMENTR but rapidly instar. it rapid declir levels seen -!- SIMILARITY: hydrolases).	This This The the twee and anodi	DR EMBL; U02270; AAC04924.1; DR EMBL; L49234; AAB3952.1; DR PIR; A56596; A56596. DR InterPro; IPR002557; Chitin bind PerA. DR TinterPro; IPR01223; Glyco hydro 18.
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Euteleostomi;

FUNCTION, AND SUBCELLULAR

(ISOFORMS 1 AND 2),

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SEQUENCE OF 22-42 AND 178-198, FUNCTION, AND TISSUE SPECIFICITY.
MEDLINE=95138187; PubMed=7836450;
Renkema G.H., Boot R.G., Muijsers A.O., Donker-Koopman W.E.,
Aerts J.M.F.G.;
"Purification and characterization of human chitotriosidase, a novel
member of the chitinase family of proteins.";
J. Biol. Chem. 270:2198-2202(1995).
                                                                                                                                            "Cloning of a cDNA encoding chitotriosidase, a human chitinase produced by macrophages.";
J. Biol. Chem. 270:26252-26256 (1995).
                                                                                                                                                                                                                                                                                                             MEDLINE=98421482; PubMed=9748235;
Boot R.G., Renkema G.H., Verhoek M., Strijland A., Bliek J., de Moulemeester T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G. Menulemeester T.M.A.M.O., Mannens M.M.A.M., Aerts J.M.F.G. "The human chitotriosidase gene. Nature of inherited enzyme
                                                                                               TISSUE=Macrophage;

BOOT NE=96064655; PubMed=7592832;

BOOT RG, Renkema G.H., Strijland A., van Zonneveld A.J.,

Aerte J.M.F.G.;
          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                   POLYMORPHISM, AND DESCRIPTION OF ISOFORM 3.
                                                                      SEQUENCE FROM N.A.
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  deficiency
412
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                                                                                                                                                                                                                                                                                                                                                                                                                    GAMTWAIDMDDFGGLGGEKNPLIKILHKHMS------SYTVPPPHTENTTPTP
                                                                                                                                                                                                                                                                                                    10 SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDD
                                                                                                                                                                                                                                                                                                                                                      69 NHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQSVLDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 YLNNGATRDKLVMGVPFYGRAWSIED------RSKLKLGDPAKGMSPPGFISGEE
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                                                                                                                                                                                                                                                                             Gaps
           Pfam; PF00704; Glyco hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SWART; SM06894; GhtBD2; 1.
SWART; SM00636; Glyco_18; 1.
PROSITE; PSS0940; CHIT BIND_II; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                    SER/THR-RICH.
CHITIN-BINDING TYPE-2.
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                            84;
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                                                                                                                                                                                                                                                                             202; Indels
                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                           3989D756C96CD490 CRC64;
                                                                                                                                                                                                                                                   27.7%; Score 834; DB 1;
35.9%; Pred. No. 1.3e-38;
tive 76; Mismatches 202;
                                                                                                                          ENDOCHITINASE.
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                                                                                                                                                                                                                            62203 MW;
                                                                                                                                                                                                                                                                             Conservative
   PF01607; CBM 14; 1.
                                                                                                                19
5554
4553
553
146
407
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Best Local Similarity
Matches 203; Conserv
                                                                                                   Gîycoprotein.
SIGNAL
CHAIN
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SEQUENCE
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                                                                                                                                       DOMAIN
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   Pfam;
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Biol. Chem. 273:25680-25685(1998)

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but
                       CHITOBIOSE AND ALLOGAMIDIN.

MEDLINE=22095530; PubMed=11960986;

Fusetti F., von Moeller H., Houston D., Rozeboom H.J., Dijkstra B.W.,

Boot R.G., Aerts J.M.F.G., van Aalten D.M.F.;

"Structure of human chitotriosidase. Implications for specific
inhibitor design and function of mammalian chitinase-like lectins.";

J. Biol. Chem. 277:2553-2544(2002).

-!- FUNCTION: Degrades chitin and chitotriose. May participate in the
defense against mematodes and other pathogens. Isoform 3 has no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOLYMORPHISM: A 24 bp duplication in exon 10 leads to the activation of an alternative splice site and the production of an inactive procein. About 6% of the population are deficient for CHIT1 activity, while 35% are carriers and show reduced enzyme levels. People with CHIT1 deficiency appear perfectly healthy. MISCELLANEOUS: Patients with type I Gaudher disease (GD 1) [MIM:230800] have very high plasma levels of CHIT1, and this can be used as diagnostic aid and to evaluate the success of treatment. Successful therapy brings the CHIT1 activity levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Secreted. A small proportion is lysosomal.
-i- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=Q13231-3; Sequence=VSP_008633;
Note=Duplication of 24 bp in exon 10 leads to the use of a
cryptic splice site. The normal splice site is still present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Detected in spleen. Secreted by cultured
                                                                                                                                                                                                                                                                                                                                                                                                                    jo
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-386 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                 enzymatic activity.
CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSP 008632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               chitin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q13231-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl-D-glucosamine polymers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Monomer.
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CHT1 HUMAN STANDARD, PRT; 466 AA.
Q13211, Q9H3V8;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chitotriosidase 1 precursor (RC 3.2.1.14) (Chitinase 1).

CETTTE C

HUMAN

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Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                  CHIA_MOUSE
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 -EKRGYERFINILALKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIOSVLDFLOEYK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 NDETLYQEFNGLKKNNPKLKTLLAIGGWNFGTQKFTDWVATANNRQTFVNSAIRFLRKYS 131
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REAL GO: GO: 0005615; C: extracellular space; TAS.

GO: GO: 00045615; C: extracellular space; TAS.

GO: GO: 00045617; P: response activity; TAS.

GO: GO: 0009617; P: response to bacteria; TAS.

REAL GO: GO: 0009613; P: response to pest/pathogen/parasite; TAS.

InterPro: IPR001257; Chitin bind PerA.

RITERPRO: IPR001257; Chitin bind PerA.

RITERPRO: IPR001257; CHM 14; 1.

REAL SPOOLOGY: GBM 14; 1.

REAL SPOOLOGY: GBM 14; 1.

REAL SPOOLOGY: GBM 14; 1.

REAL SMO0449; Chror 18; 1.

REAL SMO0499; CHRTINASE 18; 1.

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REAL SMO0495; CHITINASE 18; 1.

REAL SMO0405; CHITINASE 18; 1.

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REAL SMO0405; CHITINASE 18; 1.

REAL SMO04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
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Pred. No. 1.8e-33;
5; Mismatches 150; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SL -> NG (in isoform 2).
/FIId=VSP 008631.
Missing (In isoform 2).
/FIId=VSP 008632.
Missing (In isoform 3).
/FIId=VSP_008633.
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CHITIN-BINDING TYPE-2.
BY SIMILARITY.
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EMBL; U62662; AAG10644.1; --
EMBL; UG47, 31-JAN-02.
PDB, 11G1; 18-SEP-02.
PDB, 11G2; 18-SEP-02.
PDB, 11G0; 29-JUJ-03.
Genew; HGNC:1936; CHITI.
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417
140
26
307
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DISULFID
DISULFID
VARSPLIC
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUE=Stomach;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,

Rochim L.M., Scaubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

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Brownstein M.J., Bult C., Fletcher C., Falli J., Mombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

Nurahiaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanahiaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanahiaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
310 KGATKQRIQ-DQ--KVPYIFRDNQWYGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366
                                                                                   425
                                                                                                                                      G-----RYPLIQTLRQELSLPYLPSGT 394
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MEDLINE=22388257; PubMed=1247932;
MEDLINE=22388257; PubMed=1247932;
MEDLINE=22388257; PubMed=1247932;
MISTERE S.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,
Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                   GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTPTTTPTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boot R.G., Blommaart E.F.C., Swart E., Ghauharali-van der Vlugt K., Bijl N., Moe C., Place A., Aerts J.M.F.G., "Identification of a novel acidic mammalian chitinase distinct from chitotriosidase.";
                                                                                                                                                                                                                                                                                                                                                                                                            Q91XÄ9; Q99PH2; Q9D803; Q9TLN1;
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last anguence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase) (YNL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rođentia, Sciurognathi; Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., SEQUENCE OF 22-43, TISSUE SPECIFICITY, AND
                                                                                                                                                                                                                                                                                                                                                                                      473 AA
                                                                                                                                                                                           426 PSPTTPTTPSPTTTPSPTTPT 450
                                                                                                                                                                                                                                                395 PELEVP-KPGQPSEPEHGPSPGQDT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Lung;
MEDLINE=21125893; PubMed=11085997;
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191

366

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247 INNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLF 306
                                                                                                                                                                                                                                                                307 QK---EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDD 363
 74 EKRGYERFINILRLKNPELTTMISLGGWYEGSEKYSDWAANPTYRQOFIOSVLDFLQEYKF 133
                                                                                                                                                   187 DRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYY
                                                                                                                                                                                                                                                                                    : | | : | | : | | : | | : | | | : : | | | SGATEVW----DASQEVPXAXKANEWLGYDNIKSFSVKAQWLKQNNFGGAMIWAIDLDD
                                                                  DGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG------YLLTAAVSPGKDKI
                    364 FKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTPTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R EMBL; AK008633; BAB25795.1; ...
R EMBL; BC011134; AAH1114-1; ALT_INIT.
R EMBL; BC01134; AAH3164-1; ALT_INIT.
R EMBL; BC01134; AAH3164-1; ALT_INIT.
EMBL; AF154571; AAF31644-1; ALT_INIT.
EMBL; AF154571; AAF31644-1; ALT_INIT.
R MGD; MG1:1932052; Chia.
R MGD; MG1:1932052; Chia.
R MGD; MG1:1932052; Chia.
R MGD; MG1:1932052; Chitin bind Perry
R GO; GO:0006032; P:chitin bind Perry
R InterPro; IPR001237; Glyco_hydro_18.
InterPro; IPR001237; Glyco_hydro_18.
InterPro; IPR001799; Glyco_hydro_18.
R Pfam; PF01074; Glyco_hydro_18; 1.
R ProDom; PF00677; Glyco_hydro_18; 1.
R SWART; SM00636; Glyco_hydro_18; 1.
R RNSITE; PS01095; CHIT BIND II; 1.
R RNSITE; PS01095; CHIT BIND II; 1.
R PROSITE; PS01095; CHIT BIND II; 1.
R PROSITE; PS01095; CHIT MASE 18; 1.
R PROSITE; PS01095; CHIT MASE 18; 1.
R POLYAGACHARIGE GEGRAGATION; Hydrolase; Glycosidase; Chitin-binding; PS01095; CHIT MASE 18; 1.
R POLYAGACHARIA CHIT MASE 18; 1.
R POLYAGACHARIGE GEGRAGATION; Hydrolase; Glycosidase; Chitin-binding;
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                              Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACIDIC MAMMALIAN CHITINASE.
CHITIN-BINDING TYPE-2.
BY SIMILARITY.
BY SIMILARITY.
F -> A (IN REF. 1).
W, 333C874477476695 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 727.5; 37.0%; Pred. No. 6.7
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                                                                                                                                                                                   SEQUENCE OF 2-473 FROM N.A.
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22
424
140
140
367
307
293
473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      hydrolases)
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                                                                                                                                  and mouse
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     407
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MEDLINE=22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl-D-glucosamine polymers of chitin.
FTGSFCDQGKFPLTSTLNKA-------LGISTEGCTAPDVPSEPVTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heterochromatic sequences in a Drosophila whole-genome shotgun
                                                                                                                                                                                                                                                                                                                               0995503 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
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in Aedes, Anopheles and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF026500; AAB81858.1; -. FlyBase; FBgn0022703; Chtl.
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                                                                                                                                                                                                                                                                                                  STANDARD;
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11; 73 72

49;

Indels

69; Mismatches 144;

Conservative

Similarity

Best Local Simi Matches 154;

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16 IVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW-

24 LICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNNEITT---

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Chem. 276:6770-6778(2001).
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    194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 VIDAGYEVAELSHYFSWISVMAYDYHGQMDKKTGHVAPMYSHPEGT----ANFNANFSMN 367
                                                                                                                                                                                                                                                                                                                                                                                                                      ---EKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDMAANPTYRQQFIQSVLDFLQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 EYNFDGLDLDWBYPVCWQVDCKKGTAE-EKIGFSALVRELFYAFQPRGLILSAAVSPNKK 311
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                                                                                                                                                                                                                                                                                                                                                                     143 KIICYFTNWAWYRQGGGKFLPEDIDSDLCTHIIYGFAVLSRDNLTIQ------PHDSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 LFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDD
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MEDLINE=21125893; PubMed=11085997;
MEDLINE=21125893; PubMed=11085997;
Bijl N., Moe C., Place A., Aerts J.M.F.G.;
"Identification of a novel acidic mammalian chitinase distinct from chitotriosidase.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=20018184; PubMed=10548734;
Saito A., Ozaki K., Fujiwara T., Nakamura Y., Tanigami A.;
"Isolation and mapping of a human lung-specific gene, TSA1902, encoding a novel chitinase family member.";
Gene 239:325-331(1999).
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Propon; PR00704; Glyco_hydro_18; 2.
SWART; SW00634; Glyco_hydro_18; 2.
SWART; SR00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Hydrolase; Glycosidase; Chitin degradation; Multigene family.
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99BZE6; Q9BZE6; Q9ULY4;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
45-MAR-2004 (Rel. 43, Last annotation update)
Acidic mammalian chittinase precursor (EC 3.2.1.14) (AMCase)
(TSA1902).
                                                                                                                                                              264 264 PROTON DONOR (BY SIMILARITY)
508 AA; 57751 MW; 26CA23B02EFDEE97 CRC64;
                                                                                                                                                                                                                              tch
24.0%; Score 723; DB 1; Length 50
al Similarity 39.8%; Pred. No. 1.3e-32;
144; Conservative 71; Mismatches 121; Indels
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                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                              ACT SITE
SEQUENCE
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RA MEDISHE-2238827; PubMed=12477932;

RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Bichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Branchein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,

RA Branchein M.J., Widin T.B., Tochiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hals, Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hallow, Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Hiking M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakealey R.W., Tuckman J.W., Green B.D., Dickson M.C.,

RA Blakealey R.W., Krzywinski M.I., Skalaka U., Smailus D.E.,

Ratherfield Y.S.M., Krzywinski M.I., Skalaka U., Smailus D.E.,

Ratherfield Y.S.M., Krzywinski M.I., Skalaka W.A.;

Rochert on and initial analysis of more than 15,000 full-length human

Ratherfield C.D.A. Reconstront M. P. Decker Construction and initial analysis of more than 15,000 full-length human

Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Ratherfield R.M. Rather
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-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl hydrolases).
-!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!-FUNCTION: Degrades chitin and chitotriose. May participate in the defense against nematodes and other pathogens.
-!-CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-!-SUBCELLULAR LOCATION: Secreted (Probable). Isoform 2 and isoform 3 lack the signal sequence and are cytoplasmic.
-!-ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
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EMBL; AB025009; BAA86980.1; --
EMBL; AF290004; AA66019.1; --
EMBL; BC47336; AA447336.1; ALT_INIT.
MIM; 606080; --
GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0006586; F:chitinase activity; NAS.
GO; GO:0006030; P:chitin metabolism; NAS.
InterPro; IPR001257; Chitin bind Pera.
InterPro; IPR00123; Glyco hydrolism; Pfam; Pf00167; CBM 14; 1.
Pfam; Pf00167; CBM 14; 1.
Pfam; Pf001041; Glyco hydroll8; 1.
Probom; Pp000411; Glyco hydroll8; 1.
N.A.
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glycosyl

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SET TERT TERT SOLUTION SELECTION SEL

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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 LDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDKIDR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AYDIKELNKLEDWANVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 G-YERFUNILRIKNPELITMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 CYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKR
Insect Mol. Biol. 7:233-239(1998).
-i- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
                                                                                                                                                                                                                              EMBL; U42835; AAA83886.1; -.

R EMBL; AF026152; AAA83886.1; -.

R EMBL; AF026152; AAA83886.1; -.

R PIR; T15408; T15408.

R PIR; T15408; T15408.

R InterPro; IPR001253; Glyco_hydro_l8.

R InterPro; IPR001253; Glyco_hydro_l8.

R Pfam; PF01070; CBM 14; 2.

R Pfam; PF01070; CBM 14; 2.

R Pfam; PF01070; CBM 14; 2.

R PRART; SM00494; ChtBD2; 2.

R SMART; SM00494; ChtBD2; 2.

R SMART; SM00494; ChtBD2; 2.

R SMART; SM00494; ChtBD2; 2.

R PROSITE; PS50940; CHTT BIND II; 2.

R PROSITE; PS50940; CHTT BIND II; 2.

R PROSITE; PS50940; CHTT BIND II; 2.

R PROSITE; PS50940; CHTTN-BINDING TYPE-2 2.

T DOMAIN 563 GLYCORIDONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 617;
                           acetyl-D-glucosamine polymers of chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                              hydrolases).
SIMILARITY: Contains 2 chitin-binding type-2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W -> C (IN REF. 2).

ITF -> TTS (IN REF. 2).

I -> L (IN REF. 2).

DDA1DZAACOES4DA GRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210;
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30.2%; Pred. No. 1.4e-31;
iive 90; Mismatches 210
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178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::||| :||::| || :| || 308
250 WKDNGAPAEKLIVGFPTYGHNFILSNPSNTGIGAPTSGAGPAGPYAKESGIWAYYEIC-T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - EKRGYERFUNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQSVLDFLQBYK 132
                                                                                                                                                                                                                                                                                                                                                                                                        FDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 185
                                                                                                                                                                                                                                                                                                                        73
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                                                                                                                                                                                                                                                                                                                                             RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-HCGP-KNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTTTF 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                          23.5%; Score 708.5; DB 1; Length 476; 35.9%; Pred. No. 7.2e-32; tive 75; Mismatches 154; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 62-178 FROM N.A. MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y., Robbins P.W.; "Chitinases are a multi-gene family in Aedes, Anopheles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nhan M.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                     CHITINASE
                                                                                                                                                                                                                   92B27BAD2F7EB4CC CRC64;
                   BY SIMILARITY.

ACIDIC MAMMALIAN CHITINA
CHITIN-BINDING TYPE-2.
POLY-SER.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSING (in isoform 3).
/FTId=VSP_008634.
                                                                                                                                                              Missing (In isoform 2)
/FTId=VSP 008635.
I -> V (IN REF. 1).
V -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIT CABEL

ID CHIT CAEL

AC 01174; 017321;

DT 01-N0V-1997 (Rel. 35, Created)

DT 01-N0V-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Probable endochitinase (EC 3.2.1.14).

GN CHT-1 OR C04F6.3.

CRenorhabditis elegans.

OS Caenorhabditis elegans.

Paloderinae; Caenorhabditis.
                                                                                                                                                                                                                                52271 MW;
         splicing
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                  339
                                                                                                                                                                   108
                           21
476
476
140
150
161
                                                                                                                                                                                                                 432
        Signal; Alternative SIGNAL 1
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476 AA;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                     22
427
415
140
307
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CONFLICT
SEQUENCE
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                                                                    DOMAIN
ACT SITE
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248 287 308 346

135

113 92

Gaps

406

456

405

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STRAIN=Merino; TISSUE=Oviduct;

MEDLINE=96329120; PubMed=9726811;

MEDLINE=96329120; PubMed=9726811;

Marshall J.T.A., Nancarrow C.D., Brownlee A.G.;

Marshall J.T.A., Nancarrow C.D., Brownlee A.G.;

Marshall J.T.A., Nancarrow C.D., Brownlee A.G.;

To centrus—associated oviducal protein.";

Reprod. Fertil. Dev. 8:305-310(1996.

- FUNCTION: Binds to cocyte Sona pellucida in vivo. May play a role

in the fertilization process and/or early embryonic development.

- INDECLIDIAR LOCATION: Secretory granules.

- SUBCELIDIAR LOCATION: Secretory granules.

- TISSUE SPECIFITY: Oviduct.

- DEVELOPMENTAL STAGE: Levels are highest in the fimbria and ampulla at estrus and on day 1 of pregnancy, when gamete transport and fertilization occurs in the E2-dominated fallopian tube. Levels decline significantly on day 2 and undergo a further significant
                                                                                                                                                                                     QAGFLAYYEVCSFVQRAKKRW---IDHQY-VPYAYRGKEWVGYDDDISFSYKAFFIKKEH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 CPESLAVŤKDLŤTDLGILPLGGEAVAŤEŤHGRŠDNM-ŤVŤPGGGLVAPŤRPTLSFGKLŤV 465
K-----DARD--ESIFYPEFNQLKERNEKLKTLLSIGGWNFGTSRFTTMLSTFTNREK 119
                                                                                349 FGGAMWWILDLDDVRGTFCGTGPFPLVYMINDL--LLKABVSSTLSPGFGLSTTVNSSRT
                                                                                                                                                      173 YLLTAAVSPGKDKIDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDE
                                                                                                                                                                                                                                                         233 LHTYFNVNYTWHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISG
                                                                                                                                                                                                                                                                                                                                                           EBGVLSYIELCOLFO -- KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 VSGVMVWSLENDDFKG-HCG----PKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028542; 028543;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 39, Last annotation update)
04-NOV-1997 (Rel. 39, Last annotation update)
0viduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Estrus-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desouza M.M., Murray M.K., "An estrogen-dependent secretory protein, which shares identity with chitinases, is expressed in a temporally and regionally specific manner in the sheep oviduct at the time of fertilization and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APEGKTESPGEKAMTPVGHPSVTP
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MEDLINE=95269691; PubMed=7750470;
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OVGP1 OR OGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 10-539 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9940;
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          69
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OGP_SHEEP
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                                                                                        -----PITIPSPITIPSPITIPSPITPITPAPITSTPSPITTEHISEIPKYTIYVDGH 484
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Buhi W.C., Alvarez I.W., Choi I., Cleaver B.D., Simmen F.A.;
"Molecular cloning and characterization of an estrogen-dependent porcine oviductal secretory glycoprotein.";
Biol. Reprod. 55:1305-1314 (1396).
-: FUNCTION: Binds to cocyte zona pellucida in vivo. May play a role in the fertilization process and/or early embryonic development.
-: SUBCELLULAR LOCATION: Secretory granules.
-: TISSUE SPECIFICITY: Oviduct.
-: SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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                                    TTAATTTTTRAATTTTTASNTNVCSGKSDGFYPNSNNCGLFVLCLSSKSYSMSCPSGLQYS
                                                                                                                       519 ASLKXCTTSTASGCSVTTTRAPTTTKSAPT--VTTTTRAPTTT-----TPAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (POSP-B3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
31B78F49CA2363A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                    --KCIKDGFFGVPSDCLKFIRC--VNG--ISYNFECPNGLSFHADIWMC 607
                                                                                                                                                                                        LIKCYKEGDIPHPINIHKYLVCEPVNGGWWVHIMPCPPGTIWCQEKLTC 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
STRAIN=Yorkshire X Duroc X Hampshire, TISSUE=Oviduct;
MEDLINE=97107140; PubMed=8949888;
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InterPro; IPR001579; Glyco hydro 18AS.
Prom. PP00049; Glyco hydro 18; 1.
SMART; SM00636; Glyco hydro 18; 1.
SROSITE; PS01095; CHITINAEE 18; FALSE NEG.
Glycoprotein; Fertilization; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                        527 AA
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Pred. No. 4.7
                                                                                                                                                                                                                                                                                                                                                                        PRT;
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34.9%;
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                                                                                                                                   Mus musculus
                                         C3L1 MOUSE
Q61362;
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSYIELCOLFQKEEWHIQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGVMV 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAVSPGKDKIDRAYDIKELNKLFDWMVMIYDYHGGWENFYGHNAPLYKRPDEIDELHIY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 -SSAYAMSYWRQLGVPPEKLLMGLPTYGRTFHLLRASQNELGAGAAGPASPGKYTKQAGF 296
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
coincident with transport of the
 reduction on day 3 of pregnancy coincident with transport of embryo from the oviduct to the uterus, a reproductive stage associated with rising progesterone levels.
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                     . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 682.5; DB 1; Length 539; 34.4%; Pred. No. 2.2e-30; Live 85; Mismatches 180; Indels 61
                                                                                                                                                                                                                                                                             SPECIFIC GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                    M -> V (IN REF. 2).
K -> N (IN REF. 2).
A -> V (IN REF. 2).
A -> V (IN REF. 2).
R -> H (IN REF. 2).
R -> H (IN REF. 2).
R -> H (IN REF. 2).
M, F35000269987C193 CRC64;
                                                                                                                                                           EMBL; U17988; AARO1052.1; -.

PIR; 146470; 146470.

InterPro; 1PR001223; Glyco_hydro_18.

InterPro; 1PR001223; Glyco_hydro_18.

InterPro; PR001579; Glyco_hydro_18.

ProDon; PR000471; Glyco_hydro_18; 1.

SMART; SM00636; Glyco_18; 1.

PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

Glycoprotein; Fertilization; Signal.

SIGNAL

2 539 OVIDUCT-SPECIFIC

CHAIN
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539 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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Morrison B.W., Leder P.;
"neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
Oncogene 9:3417-3426(1994)
-;-FUNCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 EWNDESNYDKLAKTRATRATALKTLLSVGGWKFGEKRFSEIASNTERRTAFVRSVAPFLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 YGFDGLDLAWLYPRLR-----DKOYFSTLIKELNAEFTKEVQPGREKLLLSAALSAGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 KLVCYFTSWSQYREGVGSFLPDAIQPFLCTHIIYSFANIS------SDNMLSTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Gaps
                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39)
(GP-39) (BRP39 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
subcclluda LoCATION: Extracellular (By similarity).
subclludar LoCATION: Extracellular (By similarity) hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 680; DB 1; Length 38 37.1%; Pred. No. 2e-30; tive 75; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 21 POTENTIAL.
22 381 CHITINASE-3 LIKE PROTEIN 1.
60 60 N-LINKED (GLCNAC. . ) (POT
381 AA, 43001 MW; EF6581E8184F0450 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001223; Glyco hydro_184.
InterPro; IPR001579; Glyco_hydro_187.
Pfam; PF00704; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
381
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Breast;
MEDLINE-95060797; PubMed-7970700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X93035; CAA63603.1; -.
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MGD; MGI:1340899; Chi311.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal
                                                                                                                                                                                                                                                                       (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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FDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 185
                                                                                                                  23 KLVCYFTNWA-HSRPGPASIMPHDLDPFLCTHLIFAFASMSNNQI---VAKNLQDENVL- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OVGP1 OR OGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGP MESAU
                                                                                                                                                                                                                                             246
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OGP MESAU
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10. Reprof. 53:285-294(1995).

11. Eloi. Reprof. 53:285-294(1995).

12. In the fertilization process and/or early embryonic development.

13. SUBCELLULAR LOCATION: Secretory granules.

14. SUBCELLULAR LOCATION: Secretory granules.

15. SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

16. SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

17. SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

18. SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

19. SIMILARITY: Belongs to family 18 of glycosyl hydrolases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 YMIRLGAQASKLIMGIPTFGKSFTLAS-SENQLGAPISGEGLPGRFTKEAGTLAYYBICD 302
       245 YYLNNGATRDKLVMGVPFYGRAMSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 304
                                                             305 LFQKEEWHIQYDEYYNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGVMYWSLENDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and characterization of a mouse oviduct-specific
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Betrogen-dependent oviduct protein).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendai Y., Komiya H., Suzuki K., Onuma T., Kikuchi M., Hoshi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
37246C8F01665552 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%; Score 680; DB 1; Length 721; 33.7%; Pred. No. 4.1e-30; ive 79; Mismatches 184; Indels
                                                                                                                                                                                                                     721 AA
                                                                                                                                     KGHCGPKN--PLLNKVHNMI 382
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469
721 AA;
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                                                                                                 GTFCGNGPFPLVHILNELLVQTESNS-----TPLPQFWFTSSVNASGPGSENTAL 413
                                                                                                                                                    306 PQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 365
                                                                                                                                                                       306 VQRAKKG--WIDYQYVPYAFKGKEWLGYDDTISFSYKAMYVKREHFGGAMVWTLDMDDVR 363
                     414 TEVLTTDTIKILPPGGEAMTTEVHRRYENMTTVPSDGSVTPGGTASPRKHAVTPENNTMA
                                                                                                                                                                                                                                                                                                        186 IDRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0605577 060526;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
0viduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (ZP-0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Oviduct;

BIGDLINE=S05115007; PubMed=7492686;
Suzuki K., Sendai Y., Onuma T., Hoshi H., Hiroi M., Araki
Suzuki K., Sendai Y., Onuma T. Hoshi H., Hiroi M., Araki
"Molecular characterization of a hamster oviduct-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                     451 PITPIP-----APITSIPSPITI---EHISEIPKYIIVV 481
                                                                                                                                                                                                                                                                                                                                                                                                                          474 AEAKTMSTLDFFSKTTTGVSKTTTGISKTTTGVSKTTTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 14-671 FROM N.A., AND REVISIONS. TISSUE=Oviduct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96192955; PubMed=8607967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein.";
Biol. Reprod. 53:345-354(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Conservative

Best Local Similarity Matches 175; Conserv

82;

245

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                                                                                                                                                                                                               246 YLNNGATRDKI,VMGVPFYGRAWSIEDRSKI,KI,GDPAKGMSPPGFISGEEGVI,SYIELCQL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTFCGNGPFPLVHILNELLVRAEFNSTPLPQFWFTLPVNSSGPGSESLPVTEELTTDTVK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 ILPPGGEAMATEVHRKYEKVTTIPNGGFVTPAGTTSPTHAVALERNAMAPGAKTTTSLD 483
PDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 185
                              ||||||| : ||| |-|| |-| |-| |-| |-| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |-|| |
                                                                                                                                                                                                                                                      FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVNVWSLENDDFK
                                                                                                                                                                                                                                                                                                                                                           G-HCG-PKNPLLNKVHNMINGDEKNS-----FECILGPSTTTPTPTTTTPTTPTTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Reprod. 50:927-934(1994).
-!- FUNCTION: Binds to cocyte zona pellucida in vivo. May play a rollin the fertilization process and/or early embryonic development.
-!- SUBCELLULAR LOCATION: Sortetory granules.
-!- TISSUB SPRCIFICITY: Oviduct.
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oviduct-specific glycoprotein precursor (Oviductal glycoprotein) (Oviductin) (Estrogen-dependent oviduct protein) (Fragment). OVGP1 OR OGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=0viduct;
MEDLINE=94257768; PubMed=8199272;
Sendai Y., Abe H., Kikuchi M., Satch T., Hoshi H.;
"Purification and molecular cloning of bovine oviduct-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 --SPITPTPTPAPITSTPSPITTEHTSETP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 LLSETMIGMIVIVQTQIAGRETMITVGNQSVIP 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 19-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S57197; S57197; InterPro; IPR001223; Ilyco hydro 18. InterPro; IPR001579; Glyco hydro_18AS. Pfan; Pf00704; Glyco hydro_18; I. ProDom; PD000471; Glyco hydro_18; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D16639; BAA04065.1; -.
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028042;
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                                       MEDLINE=94058981; PubMed=8240241;
Malette B., Bleau G.;
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Malette Garlilatation of hamster oviductin as a sulphated rong process and/or early embryonic development.
Might act as a protective secretion influencing the first steps of the reproductive process necessary for the normal triggering of the reproductive process necessary for the normal triggering of the reproductive and early embryonic development.

C.:- SUBCLINIAR LOCATION: Secretory granules.
C.:- TISSUE SPECIFICITY: Oviduat.
C.:- PITM: HIGHLY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED.
C.:- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVIDUCT-SPECIFIC GLYCOPROTEIN.
8 X 15 AA TANDEM REPEATS.
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H -> I (IN REF. 4).
D -> G (IN REF. 2 AND 3).
R -> Q (IN REF. 2 AND 3).
F -> Y (IN REF. 2 AND 3).
Q -> L (IN REF. 2 AND 3).
MISSING (IN REF. 2 AND 3).
T -> I (IN REF. 2 AND 3).
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-> I (IN REF. 2 AND 3).
BB57E0E514EC1972 CRC64;
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InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001229; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
ProDom; P0000471; Glyco hydro 18; 1.
SMART; SM00365; Glyco hydro 18; 1.
SMART; SM00365; Glyco 18; 1.
Glycoprotein; Fertilization; Repeat; Signal.
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Matches 175; Conservative
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671 AA;
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FROM N.A., AND VARIANT GLN-676.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGP HUMAN STANDARD; PRT; 678 AA.

Q12889; Q15841;
01-NOV-1997 (Rel. 35, Created)
10-OCT-2003 (Rel. 35, Last sequence update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Mucin 9).
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                                                                                                                                       (POTENTIAL)
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TISSUE=Oviduct;
MEDLINE=95119256; PubMed=7819450;
Arias E.B. Verhage H.G., Jaffe R.C.;
"Complementary deoxyribonucleic acid cloning and molecular characterization of an estrogen-dependent human oviductal
                                                                                                         OVIDUCT-SPECIFIC GLYCOPROTEIN.
N-LINKED (GLCNAC. . .) (POTENT
CPDCEE6F0212D791 CRC64;
                                                                                                                                                                                                                     Query Match 22.3%; Score 673; DB 1; Length 53
Best Local Similarity 33.7%; Pred. No. 7.1e-30;
Matches 170; Conservative 90; Mismatches 179; Indels
PROSITE; PSO1095; CHITINASE 18; FALSE NEG.
Glycoprotein; Fertilization; Signal.
NON TER
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Biol. Reprod. 51:685-694(1994)
[2]
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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                                                                                                                          Coville G.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds to occyte zona pellucida in vivo. May play a ro!
in the fertilization process and/or early embryonic development
-!- SUBCELLULAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: Oviduct.
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BY SIMILARITY.
OVIDUCT-SPECIFIC GLYCOPROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
F -> Q (in dbSNP:7825).
F -> Q (in dbSNP:7825).
M -> T (IN REF. 2).
S -> P (IN REF. 2).
Y -> H (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases
Jaffe R.C.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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GO: 0007565; P: pregnancy; TAS.
InterPro; IPR00123; Glyco hydro_18.
InterPro; IPR00123; Glyco hydro_18.
Pfam; PF00704; Glyco hydro_18; 1.
Probom; PD000401; Glyco hydro_18; 1.
PROSITE; PS01095; CHITINASE 18; FALSE NEG.
Glycoprotein; Pertilization; Signal, Polymory SIGNAL
CHAIN
22 678
OVIDUGI-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; US8010; AAB04126.1; --
EMBL; US8001; AAB04126.1; JOINED.
EMBL; US8002; AAB04126.1; JOINED.
EMBL; US8003; AAB04126.1; JOINED.
EMBL; US8003; AAB04126.1; JOINED.
EMBL; US8005; AAB04126.1; JOINED.
EMBL; US8006; AAB04126.1; JOINED.
EMBL; US8007; AAB04126.1; JOINED.
EMBL; US8008; AAB04126.1; JOINED.
EMBL; US8009; AAB04126.1; JOINED.
EMBL; US8009; AAB04126.1; JOINED.
EMBL; US8009; AAB04126.1; JOINED.
EMBL; US8009; AAB04126.1; JOINED.
EMBL; US8009; AAB04126.1; JOINED.
EMBL; AL390195; CAC36039.1; --
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                                                                                                                                                                                         EMBL, M80927; CAAG6661.1; --
EMBL, Y08374; CAAG9661.1; --
EMBL, Y08375; CAA69661.1; JOINED.
EMBL, Y08377; CAA69661.1; JOINED.
EMBL, Y08377; CAA69661.1; JOINED.
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SIGNAL 1
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PDB; 1LA7; 10-APR-02
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P36718;
01-JUN-1994
01-NOV-1997
15-JUL-1999
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AAVSPGKOKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTY 236
                                                       237
                                                                                                                                                                                                                 LSYIELCOLF--OKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGV 354
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Myirkos P., Golds E.E.;

Nyirkos P., Golds E.E.;

Nyirkos P., Golds E.E.;

Nyirkos P., Golds E.E.;

Nyirkos P., Golds E.E.;

Nyirkos P., Golds E.E.;

I amamary proviein capressed during the non-lactating period.";

Blochem. J. 269:265-268(1990).

-!- FINCTION: May play an important role in the capacity of cells to respond to and cope with changes in their environment.

-!- FINCTION: May play an important role in their environment.

-!- FINCTION: May play an important role in their environment.

-!- FINCTION: May play an important role in their environment.

-!- FINCTION: May play an important role in their environment.

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-!- FINCTION: May play an important role in their environment.
                                                                                                                                          - SSAYAMNYWRKIGAPSEKLIMGIPTYGRTFRLIKASKNGLQARAIGPASPGKYTKQEGF
                                                                                                                                                                                                                                                                                                                                                         Hakala B.B., White C., Recklies A.D.; "Human cartilage gp-39, a major secretory product of articular chondrocytes and synovial cells, is a mammalian member of a chitinase
                                                                                                                                                                                                                                                                      LAYFEICSFVWGAKKHW----IDYQYVPYANKGKEWVGYDNAISFSYKAWFIRREHFGGA
                                                                                                        237 FNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGV
                              01-UTL-1993 (Rel. 26, Created)
01-UTL-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-39) (39 kDa synovial protein) (YKL-40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rehli M., Krause S.W., Andressen R., Molecular characterization of the gene for human cartilage gp-39 (CHISIL) a member of the chitinase protein family and marker for late stages of macrophage differentiation."; Genomics 43:221-225(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein family.";
J. Biol., Chem. 268:25803-25810(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97386591; PubMed=924440;
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MEDLINE=94064658; PubMed=8245017;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 KIDRAYDIKELNKLFDWMVWTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 RIVCYVGTWSVYHKVDPYTIED-IDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
InterPro; IPR001223; Glyco.hydro.l8.
InterPro; IPR001579; Glyco.hydro.l8.
Pfam; PF00704; Glyco.hydro.l8; 1.
SMART; SM00636; Glyco.l8; 1.
SMART; SM00636; Glyco.l8; 1.
PROSITE; PS01095; CHITINASE.l8; FALSE.NEG.
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N-LINKED (GLCNAC. . .) (POI
76ADD8298EEEC2D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jaffe R.C.;

"Cloning of a recombinant complementary DNA to a baboon (Papio amubis) estradiol-dependent oviduct-specific glycoprotein.";

Mol. Endocrinol. 5:356-364(1931).

-!- FUNCTICN: Binds to occyte zona pellucida in vivo. May play a role in the fertilization process and/or early embryonic development.

-!- SUBCELLULAR LOCATION: Secretory granules.

-!- SUBCELLULAR LOCATION: Secretory granules.

-!- DEVSLOPMENTAL STAGE: At the time of ovulation.

-!- DEVSLOPMENTAL STAGE: At the time of ovulation.

-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIQD-----EXILYPEPNKLKERNRELKTLLSIGGWNFGTSRFTTWLSTFANREKFIAS
                                                                                                                                                                                                                                                                                                                                                           Mavrogianis P.A., O'Day-Bowman M.B.,
                                                                                    Pario ambis (Olive baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein) (Oviductin) (Estrogen-dependent oviduct protein).
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31.2%; Pred. No. 9e-29;
ive 82; Mismatches 195; Indels 118;
                                                                                                                                                                                                                                                                                                                                                     Verhage H.G., Fazlebas A.T., Marrogianis P.A., O'Day-Bowman M.I. Donnelly K.M., Arias B.B., Jaffe R.C.; "The baboon oviduct: characteristics of an oestradiol-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91367180; PubMed-1716345;
Donnelly K.M., Fazleabas A.T., Verhage H.G., Mavrogianis P.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                oviduct-specific glycoprotein.";
Hum. Reprod. Update 3:541-552(1997).
                                                                                                                                                                                                                                                                                                  TISSUE=Oviduct;
MEDLINE=98244335; PubMed=9584944;
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Matches 179; Conserv
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ALIGNMENTS

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T14075
Cispeciaes (BC 3.2.1.14) - yellow fever mosquito
Cispeciaes. Aedes aegypti (yellow fever mosquito)
Cispeciaes. Aedes aegypti (yellow fever mosquito)
Cispeciaes. Aedes aegypti (yellow fever mosquito)
Cispeciaes. Aedes aegypti (yellow fever mosquito)
Cispeciaes. Aspeciaes. T14075
Ride la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A;Accession: T14075
A;Accession: T14075
A;Accession: T14075
A;Accession: L1635 < DBA
A;Residues: 1-1635 < DBA
A;Cross-references: EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AAB81850.1
C;Genetics:
A;Gene CHT2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         820 AFKPKGLILSSAVSPSKKVVDEGYDVVTLSDYMDWIAVMAYDYHGQMDKKTGHVAPMYEH 879
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                                468
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                                                                                                            HLIKCY--KEGDIPHPINIHKYLVC-----EFVNGGWWVHIMPCPPGTIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 28.8%; Score 869; DB 2; Length 16
Best Local Similarity 34.3%; Pred. No. 5e-46;
Matches 196; Conservative 95; Mismatches 196; Indels
TTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG--
                                                                                                                                                                ---PCAGGRYGEVPHPTNCARYYICLTADTYYEFT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 --WAYYELCTEVDKDDSGWTKKWDEQGKCPYAYKGTQWVGYEDPRSVEIKWMWIKQKGYL 365
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                                          29-Jan-1999
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                                                                                                                                                                                                                                                 A;Experimental source: larvae
A;Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 «KRA»
A;Cross-references: GB:U02270; GB:S64757; NID:g406048; PID:g406049
Chitinase (EC 3.2.1.14) - tobacco hornworm ('Species: Manduca sexta (tobacco hornworm) ('Species: Manduca sexta (tobacco hornworm) ('Accession: A56596 R.) Recquence_revision 11-Aug-1995 #text_change R.) Roccession: A56596 R.) Corpuz, L.; Choi, H.K.; Muthukrishnan, S. Insect Biochem. Mol. Biol. 23, 691-701, 1993 Affitle: Sequence of a cDNA and expression of the gene encoding A; Reference number: A56596; MuID:93357793; PMID:8353525 A; Accession: A56596
                                                                                                                                                                                                                                                                                                                               27.7%; Score 834; DB 2; Length 554
35.9%; Pred. No. 1.8e-44;
ive 76; Mismatches 202; Indels
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                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.9
hes 203; Conservative
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Best Local S:
Matches 203
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new chitinase stored in active form

28-Jul-1995 #text_change 21-Jul-2000

A53918
Chitimase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
Chistories: Chelonus sp.
Checies: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change in the characterists on the characterists of the characterists of the characterists of the characterists of new chitimas A; Title: Isolation, cloning, and characterization of new chitimas

RESULT

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C,Accession: 146470
R;DeSouza, M.M.; Murray, M.K.
Endocrinology 136, 2485-2496, 1995
A;Title: A nestrogen-dependent secretory protein, which shares identity with chitinases, and embryo development.
A;Reference number: 146470; MUID:95269691; PMID:7750470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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174 IDIDWEYPSG-----ATDMANYVALVKELKAACESEAGSTGKDRILVTAAVAAGPATIDA 228
                                                                                                                                                249 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK 308
                                                                                                                                                                            288 KGMPKEKIIVGMPTYGRGWTLANNASAINPGTSGSPAKITQYVQ-EAGVGAYFEFCEMLAN 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 estrogen dependent oviduct protein precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SSAYAMSYWRQLGVPPEKLLMGLPTYGRIFHLLRASQNELGAGAAGPASPGKYTKQAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|::::||| :::|| HDGAAH--KLVCYFTNWA-FSRFGSASILFRDLDPFLCTHLVFAFASMNNQ--IVPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 PYODDNHNSWEKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 VLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLT
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                                                                                                                                                                                                                                                        347 GATR-YWDSQSQVPYLVQGNQWWSYDDESSFANROWAYVRREGYGGAFVWTLDFDDFNAGC
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                                                                                                                                                                                                                                                                                                                                                  406 SNSNGQLYPLISVIAKELGG-----VIIPKKGGVTTAPTTVATTVTTGRPFMTSAVTT
                                                                 189 AYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN
                                                                                                                                                                                                                                     EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC
                                                                                                                                                                                                                                                                                                                      369 GPKN----PLLNKVHNMINGDEKNSFECIL---GPSTTTPT-----PTTTPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 TTAATTTTTRAATTTTASNTNVCSGKSDGFYPNSNNCGLFVLCLSSKSYSMSCPSGLQYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIKCYKEGDIPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 533
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.larity 34.4%; Pred. No. 4.7e-35;
Conservative 85; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-539 <DES>
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Best Local Similarity
Matches 171; Conserv
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C,Species: Caenorhabditis elegans
C,Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C,Accession: T15408
R,Nhan, M.
Submitted to the EMBL Data Library, December 1995
A,Description: The sequence of C. elegans cosmid C04F6.
A,Reference number: Z18346
A,Accession: T15408
A,Accession: T15408
A,Scatus: prelimbary; translated from GB/EMBL/DDBJ
A,Bolecule type: DNA
A,References: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CESP:C04F6
C,Genetics: A,Gene: CESP:C04F6.3
A,Introns: 28/1; 66/2; 504/1
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                                                                                                                                                                                                                                                                                                                                                                        YKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIKELNKLFDWMNVMTYDYHGGWENFYG-HNAPLYKRPDETDELHTYFNVNYTMHYYLNN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE 309
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                                                                                                                                                                                                                                                                                         20 SPNKVVCYPGAMSVYRQGNGKFDINGIDPTLCTHLIYSFVGVN--GKDVKVLDPWSDLPG 77
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                                                                                                                                                                                                                                                                                                                                                  NSWEKRGYERFINLLKINPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQSVLDFLQE
                                                                                                                                                                                                                                                               12 NPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 PKNPLLNKVHNMINGDEKNSFECILGPSTT---TPTPTTTPTTTPTTPSPTTP 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKYPVLKALNSVLGRGGSSS-----PAETKRKNNVPDDQPAPPRSFAEDSAPEAP 421
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                                                                                                                                                                              DB 2; Length 483;
      A,Reference number: A53918; MUID:94342256; PMID:8063715
A;Accession: A53918
A;Status: preliminary
A;Molecule type: mRNA
A;Restdues: 1-483 «KRI>
A;Cross-references: GB:U10422; NID:g533504; PIDN:AAA61639.1; PI
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                          Query Match
26.6%; Score 801.5; DB 2; Length 4
Best Local Similarity 38.0%; Pred. No. 1.6e-42;
Matches 158; Conservative 82; Mismatches 157; Indels
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Best Local Similarity
Matches 178; Conserv
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995. #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Date: 28-Oct-1995. #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Date: 28-Oct-1995. #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57-97. #sikuchi, M.; Satch, T.; Hoshi, H.
Biol. Reprod: 50, 927-934, 1994
A;Title: Purification and molecular cloning of bovine oviduct-specific glycoprotein.
A;Reference number: S57197; MUD:94257768; PMID:8199272
A;Accession: S57197
A;Accession: S57197
A;Actus: preliminary
A;Molecula type: mRNA
A;Residues: 1-537 < SEN>
A;Cross-references: EMBL:D16639; NID:g391621; PIDN:BAA04065.1; PID:d1004583; PID:g391622
C;Keywords: glycoprotein
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                           354
                                                                                   404
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                                                                                                                                           RIGPEMPTMTRDLTTGLG1LPLGGEAVATETHRKSATWTTTPRGETATPTRTPLSSGRRT 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSAYAMNYWRQLGVPPEKLIMGLPTYGRTFHILKASQNELRAQAVGPASPGKYTKQAGF
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                                                                        6 HNDYSKNPMRIVCYVGTWSVYHKVDPYTI---EDIDPFKCTHLMYGFAKIDBYKYTIQVFD
                  WSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTTTPTP----TTTPTTP
                                                                                                                TTTPSPTTPSPTTPTTP-----TTTPSPTTTTTPSPTTTTPSPTTPTTTTPSPTTPTTTT
LSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
                                                                                                                                                                                                                                                  RESULT 7
857197
oviduct-specific glycoprotein 95K precursor - bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%; Score 673; DB 2; 33.7%; Pred. No. 1.8e-34;
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                                                                                                                                                                           PAPITSTPSPITITHTS 472
                                                                                                                                                                                                      AAPEGKTESPGEKPLTS 481
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Best Local Similarity 33.74
Matches 170; Conservative
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cartilage glycoprotein gp39 precursor - human N;Alternate names: 39K synovial protein C;Species: Box sapiens (man) C;Species: Homo sapiens (man) C;Accession: A49562; S10677; A33162 C;Accession: A49562; S10677; A33162 C;Accession: A49562; White, C; Recklies, A.D. J. Biol. Chem. 268, 25803-25810, 1993 A;Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and A;Reference number: A49562; MUID:94064658; PMID:8245017
Cybacia Stylengerote and the sapiens (man)
Cybacia Stylengerote (man)
Cybacia Stylengerote (man)
Cybacia Stylengerote (man)
Cybacia Stylengerote (man)
Cybacia Stylengerote (man)
Cybaccasion: 138605
Ryarias, E.B.; Verhage, H.G.; Jaffe, R.C.
Biol. Reprod. 51, 685-694, 1994
Aytitle: Complementary deoxyribonucleic acid cloning and molecular characterization of Ayteference number: 138605, MulD:95119256; PMID:7819450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%; Score 667.5; DB 2; Length 654;
larity 33.7%; Pred. No. 5.2e-34;
Conservative 86; Mismatches 187; Indels 69.
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us-09-662-293-21.rpr

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Dreasf-regressing protein brp39 precursor - mouse (5pecies: Mus musculus (house mouse) (5pecies: Mus musculus (house mouse) (5pecies: Mus musculus (house mouse) (5,2pecies: Mus musculus) (5,2pecies: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 (5,4cession: 861551; 861550; 148271 (148271) (15,4ce) (1994 (148271) (1994 (148271)) (1994 (148271); MulD:95060797; PMID:7970700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 LQGAT--VRRPLGQQVPYATKGNQWYGYDDQESVKNKAKYLKSRQLAGAMVWTLDLDDFR 360
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73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-405 <MOR1>
A;Cross-references: EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; PID:g1085066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAF ----EP--HGYLLTAAVSPGKD
                                                                                             KFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK
                                                                                                                                                                                                                        IDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                                                                  ||||||||::::|:::::|||::|||::||::|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
                                                                                                                                                                                                                                                                                                                                                   YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL
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;2-2-405/Product: breast-regressing protein brp39 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Morrison, B.W. submitted to the EMBL Data Library, November 1995 submitted to the EMBL 051550 A;Reference number: S61550 A;Accession: S61550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: 861551
A, Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH-CGP--KNPLLNKVHNMI 382
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A; Residues: 1-245. T'
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C;Superfa
F;1-21/Do
F;22-405,
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heparin-binding glycoprotein 38K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S13.27
R;Shackelton, L.M.; Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) 1:A;Reference number: S513.7
A;Reference number: S513.7
A;Accession: S513.7
A;Accession: S513.7
A;Accession: S513.7
A;Residues: 1-383 <SHA>
A;Residues: 1-383 <SHA>
A;Cross-references: EMBL: Z47803; NID:g634097; PIDN:CAA87764.1; PID:g634098
C;Superfamily: Streptomyces chitinase chi40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIDRAYDI KELNKI FDWMVMTYDYHGGWEN FYGHNAPLYKR PDETDELHTY FNVNYTMH
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                                      Cross-references: GB:M80927; NID:g348911; PIDN:AAA16074.1; PID:g348912
   A; Residues: 1-383 < HAK>
A; Cross_references: GB:M80927; NID:g348911; FIDN:AAA16074.1; PID:g3489.
A; Cross_references: GB:M80927; NID:g348911; PIDN:AAA16074.1; PID:g3489.
B; Crohem. J. 269, 265-268, 1990
A; Title: Human synovial cells secrete a 39 kDa protein similar to a bo A; A; Recession: S10677; MUD:90328983; PMID:2375755
A; Accession: S10677
A; Molecule type: protein
A; Residues: 22-40, X', 42-45 < NY2>
C; Superfamily: Streptomyces chitinase chi40
C; Reywords: cartilage; extracellular protein; glycoprotein
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-383/Product: cartilage glycoprotein gp39 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.9%; Score 660; DB 2; Le
Best Local Similarity 37.0%; Pred. No. 7.5e-34;
Matches 141; Conservative 75; Mismatches 129;
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.larity 36.6%; Pred. No. 3.2e-33;
Conservative 77; Mismatches 130
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Best Local Similarity
Matches 139; Conserv
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Length 504;

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C'Accession: D83764

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirar Nucleic Acids Res. 28, 4317-4331, 2000

Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and § A; Racession: D83764

A,Accession: D83764

A,Scatus: preliminary

A,Molecule type: DNA

A,Residues: 1-599 <STO>
A,Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04635.1; GSPDB:GN001

A,Experimental source: strain C-125

A;Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLNKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTTTTPTTTPTTTPSPTTPT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 TIPSPITPITIPSPITPIPIPIPAPITSTPSPITIEHISEIPKYTTY----VDGHLIKC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TSETEAYDTD-----ETEETSET-EATTYDTDETEGO--EC
                                                                                                                                                                                                                                                                                                                                                                                                            76 RGYERFNNLRLKNPELTIMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDLDWEYP-GSRLGNPKIDKONYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 PDLDWEYPVGVAEEHAKLVEAMKTAFVEEAKTSGKQR-LLITAAVSAGKGTIDGSYNVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQEGVGA-YMVKGDQWYGYDNEETIRIKMKMLKEKGYGGAFIWALDFDDFTGKGCGKGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 CYYTHWAQYRDGEGKFLPGNIPNGLCTHILYAFAKVDB----LGDSKPFEWNDEDTEWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                          83 GMYSAVTKLRETNPGLKVLLSYGGYNFGSAIFTGIAKSAQKTERFIKSAIAFLRRNNFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKL PDWMIVMTYDYHGGWENFYGHNAPLYKR PDETDELHTY FIVNYTMHYYLINNGATRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 LGKNFDLLFLMSYDLHGSWEKNVDLHGKCHPTKGEVSGI-GIFNTEFAADYWASKGMPKE
                                                                                                                                                                                                                                                                                                             CYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQ-DDNHNSWEK
                         A; Accession: A38221
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Molecule: type: nucleic acid; protein
A; Residues: 1-504 < FFUI>
A; Residues: 1-504 < FFUI>
A; Cross-references: GB: M73689; NID: g156063; PIDN: AAA27854.1; PID: g156064
A; Note: sequence extracted from NCBI backbone (NCBIP: 85345)
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                     20.1%; Score 604.5; DB 2; Length 30.1%; Pred. No. 3.1e-30; ive 86; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 -YKEGDIPHPINIHKYLVCEFVNGGWWVHIMPCPPGTIW 526
A, Reference number: A38221; MUID:92179220; PMID:1542646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.5%; Score 588; DB 2; L 29.6%; Pred. No. 4.1e-29; tive 91; Mismatches 200;
                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.1%
Matches 156; Conservative
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Best Local Similarity 29.69
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
A3821
Cipitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
Cipitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
Cipitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
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Aititle: Transmission-blocking antibodies recognize microfilarial chitinase in brugian
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                                                                                                                                303 FLKGABVHRLSNE--KVPFATKGNQWVGYEDKESVKNKVGFLKEKKLAGAWCGHWIWMI- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWEKRGYERFINNIR-LKANPELTTMISLGGWYEGSEKYSDMAANPTYRQOFIQSVLDFLQE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQDLRDYEALNGIKDKKNTELKTILAIGGWRFGPAPFSAMVSTPQNRQIFIQSVIRFLRQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKFDGLDLDWEYPGSRLGNPKIDKONYLALVRELKDAFEPHG-----YLLTAAVSPGK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKIDRAYD-IKELN--KLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGV----MVWSLE 360
                                   244 YMTRLGAQASKLIMGIPTFGKSFTLAS-SENQLGAPISGEGLPGRFTKEAGTLAYYEICD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 QLMCYYTSWAKDRPIEGSFKFGNIDPCLCTHLIYAFAGWQNNEITYT------H 70
          YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKI--DEYKYTIQVFDPYQDDNHN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:M94584; NID:g202441; PIDN:AAB62394.1; PID:g202442 C;Superfamily: Streptomyces chitinase chi40 F;1-21/Domain: signal sequence #status predicted <SIG>F;22-399/Product: secretory protein YM-1 #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                        ---SSRSPIPSRMP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.2%; Score 608; DB 2; Length 39. Best Local Similarity 36.3%; Pred. No. 1.4e-30; Matches 141; Conservative 67; Mismatches 140; Indels
                                                                                                                                                                                                      361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTTP
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(strain C-125)

29;

Gaps

Indels 134;

Length 599;

DD 103 NEKSOTINVPNGTIVLGDPWIDTGKTFAGDTWDOPIAGNINGLNKLKGTNPNLKTIISVG 162 QY 99 GWYEGSEKYSDMAANPTYRQOPIGSVLDFYGGLDLWWEYPGSRLGRPKDK 154 DD 163 GW-TWANRESDVAATAATERVPANSAVPLEKYNPEDGLDLWWEYPGSRLGRPKDK 155 GWYTLLEKITEKLDAAGAVDGKYLLTIA-SGAATYAANTELAKLAALVDHNINTYD 280 209 YTLLEKITEKLDAAGAVDGKYLLTIA-SGAATYAANTELAKLAALVDHNINTYD 280 200 YTLLIGKITEKLDAAGAAGVDAKTLATIA-SGAATYAANTELAKLAALVDHNINTYD 280 201 PHOGAMOKISAHNAPLNYDPAASAAGVPDANT-FNVAAGAGHLDAGVPAAKLVLGVPFYG 339 202 GWYTLLIGKITEKLDAAGAAGVPDANT-FNVAAGAGGHLDAGVPAAKLVLGVPFYG 339 203 PHOGAMOKISAHNAPLNYDPAASAAGVPDANT-FNVAAGAGGHLDAGVPAAKLVLGVPFYG 339 204 SAWSIEDERSKLKLGDPAKGMSPPGFISGESGVLSYIELCOLPOKEBMHIQYDBYNN-370 205 RAWSIEDERSKLKLGDPAKGMSPPGFISGESGVLSYIELCOLPOKEBMHIQYDBYNN-370 206 RAWSIEDERSKLKLGDPAKGMSPPGFISGESGVLSYIELCOLPOKEBMHIQYDBYNN-370 207 JAKUPLNYABANKERISYDDAESISCKLAFLKSKGLGGAMFWELSGDRNK	
10 SKNEMRIVCYVGTWSVTHKUDDPYTIEDIDPEKCTHLANGRAK	RESULT 15 A3936 chitinase (EC 3.2.1.14) precursor - Bacillus circulans C;Species: Bacillus circulans C;Dectes: Bacillus circulans C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 15-Oct-1999 C;Accession: A3836; R;Matanabe, T: Suzuki, K.; Oyanaqi, W.; Ohnishi, K.; Tanaka, H. J. Biol. Chem. 265, 15659-15665, 1990 A;Title: Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed its evolut: A;Reference number: A38368; WUID: 90368776; PMID: 2203782 A;Accession: A38368 A;Status: preliminary A;Reference: DiA A;Residues: 1.699 cMAT> A;Rossareferences: A8:M57601; GB:JO5599; NID:g1066341; PIDN:AAA81528.1; PID:g142688 A;Residues: 1.699 cMAT> A;Rossareferences: A8:M57601; GB:JO5599; NID:g1066341; PIDN:AAA81528.1; PID:g142688 C;Superfamily: fibronectin type III repeat homology C;Reywords: glycosidase; hydrolase; polysaccharide degradation Cpuery Match Best Local Similarity 29.4%; pred: No. 2.4e-27; Matches 170; Conservative 67; Mismatches 185; Indels 156; Gaps 23; A1 SINCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKI

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March 22, 2004, 06:42:54 ; Search time 43.2018 Seconds (without alignments) 640.518 Million cell updates/sec
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3014
1 SIKRDHNDYSKNPMRIVCYV.....IMPCPPGTIWCQEKLTCIGE
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5.1.6
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 21, Application US/0929225

| Patent No. 6455686
| GENERAL INFORMATION:
| PAPPLICANT: McCAIL Catherine A. |
| APPLICANT: McDer, Eric R. |
| APPLICANT: Weber, Eric R. |
| APPLICANT: Weber, Eric R. |
| TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION NOWBER: US/09/292,225
| CURRENT FILING DATE: 1999-04-15 |
| EARLIER APPLICATION NUMBER: 60/088,295 |
| EARLIER PILING DATE: 1998-05-13 |
| EARLIER APPLICATION NUMBER: 60/089,565 |
| EARLIER APPLICATION NUMBER: 60/089,565 |
| EARLIER APPLICATION NUMBER: 60/089,295 |
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| EARLIER APPLICATION NUMBER: 60/089,295 |
| EARLIER APPLICATION NUMBER: 60

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SUMMARIES	QI	92-225-2	-09-292-2	-292-225-1	92-22	-292-225-3	92-225-3	US-08-524-051-2	9	US-09-545-814-2	-814-		US-09-545-814-32	-08-486-83	-09-151-0	-039-19	-09-343-62	-08-877-599-	-09-267-574-	-08-486-	US-09-151-011-6	3-62	US-09-039-198A-4	US-08-877-599-4	-09-267-57	9	139	-87
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1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ

100.0%; Score 3014; DB 4; 100.0%; Pred. No. 1.2e-232; iive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 536; Conservative

ORGANISM: Dermatophagoides farinae US-09-292-225-21

61 VFDFYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF

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PGKDKI DRAYD I KELNKL FDWMVMTYDYHGGWENFYGHNAPL YKRPDETDELHTYFNVN

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Sequence 15, Appl	Sequence 14, Appl	15	Sequence 29, Appl	Sequence 17, Appl	Sequence 2, Appli	4,	Sequence 2, Appli	ď	Sequence 13, Appl	ď	ť	Sequence 7, Appli	Seguence 10, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli
US-08-877-599-15	US-09-267-574-14	US-09-267-574-15	US-09-545-814-29	US-09-459-749D-17	US-08-694-915-2	US-08-694-915-4	US-08-850-348A-2	US-09-408-647A-2	US-09-052-778-13	US-09-052-778-2	US-07-939-501A-1	US-08-448-398-7	US-07-939-501A-10	US-07-939-501A-12	US-08-358-901-2	US-08-566-347-2	US-08-693-835-2
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GENERAL INTOCACHILOW:

APPLICANT: MCCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REPRENCE: AL-2-C3
CURRENT PAPLICATION NUMBER: 60/099,909
EARLIER APPLICATION NUMBER: 60/099,295
EARLIER APPLICATION NUMBER: 60/099,565
EARLIER PILING DATE: 1998-05-13
EARLIER PILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 18, Application US/09292225; Patent No. 6455686; GENERAL INFORMATION:
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Fatent No. 6455686
GENERAL INFORMATION:
APPLICANT: HUNCEY, Shirley Wu
APPLICANT: HUNCEY, Shirley Wu
APPLICANT: WEBER:
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: ALD-2-3
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ALD-2-3
FURRENT APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-04-15
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER APPLICATION NUMBER: 60/099,565
EARLIER APPLICATION NUMBER: 60/099,565
EARLIER PILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEGTRARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Dermatophagoides farinae US-09-292-225-15
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DD 363 DFKGHCOPKYPLIANKVHANNINGDEKNSYECLLGPSTTTPTPTTSTTTTPT	Ouery Match 82.1%; Score 2475; DB 4; Length 509; Bast Local Similarity 82.5%; Pred. No. 1.38-189; Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2; Cy 3 REDHUNYSKOPMEIVOYOTWSYNHKUDPYTIEDIDPFKCTHLMYGFAKIDEYKTIGVF 62 Db 22 KRDHNNYSKOPMEIVOYOTWSYNHKUDPYTIEDIDPFKCTHLMYGFAKIDEYKTIGVF 81 OY 63 DPYQDDNHNSWERHGYERFUNLELKNPELTMISLGGWYEGSEKYSDMAANFTYRQOFTO 122 [
0y 361 NDDEKGHCGPKNPLLNKVHNMINGDEKNSFECILGBETTTPTTTPTTTPTTPSFT 420 380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGBETTTPTTTPTTPTTPSFT 439 0y 421 TPTTTPSFTTPTTPSFTTPTTPSFTTPTTPTTPTTPTTPTTPTTPTTPTT 480 481 VDGHLIKCYKEGDIPHTPTTPSFTTPTTPSFTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTP	7 YPE: PRT 7 CRGANISM. Dermatophagoides farinae 0S-09-29-22-41 0uery Match 82.1%; Score 2415; DB 4; Length 490; Best Local Similarity 82.5%; Pred. No. 1.2e-189; Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2; ACHINYSKNPRIVCYOGTWSYVHYNDPYTIEDIDPFKCTHLMYGFAKIDEYKTIQVF 62 3 KEDHNYSKNPRIVCYOGTWSYTHKOPYTIEDIDPFKCTHLMYGFAKIDEYKTIQVF 62 3 KEDHNYSKNPRIVCYOGTWSYTHKOPYTIEDIDPFKCTHLMYGFAKIDEYKTIQVF 62 0 STOPYODNHNSWEKGYERPNILELKNPELITTMISLGGWYEGSEKYSDMANPTYRQOFUQ 123 SYLDFLQBYFFOGIDLDWEYPGSIGNELINKLAPEKCHLMYGFAKIDEYKTIQVF 62 0 SYLDFLQBYFFOGIDLDWEYPGSIGNELINKLAPEKCHLMYGFAKIDEYKTIQVF 62 0 SYLDFLQBYKFDGIDLDWEYPGSIGNELINKLAPEKBERFEFFGYLLTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNELNFYGHNAPLYKREDEFFFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTAAVSFG 182 0 SYLDFLQBYKFDGIDLDWEYPGSIGNENFYGHNAPLYKREDEFFFTATTFFTAFFTYFTYFYFYTY 11

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483 GHLIKCYKEGDIPHPINIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 536
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FLUE
COMPUTER: FLORY disk
MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/524,051
FILING DATE:
FLING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REGISTRATION NUMBER: 26,262
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Blvd., Suite 400 CITY: Kansas City CITY: MO COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22875-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 26,262
TELECOMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEPHONE: (816)474-9057
TELERAX: (816)474-9057
                                                                                                             Sequence 2, Application US/08524051
Patent No. 5866788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 554 amin
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amino acid
GY: linear
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                                                                              RESULT 7
US-08-524-051-2
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 DPFQDDWHNSWEKHGYERFUNLRLKNPELTIMISLGGWYSGSEKYSDMAANPTYRQQFVQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 KDKIDVAYELKELNQLEDWANVYTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFKGHCGPKYPLLNKVHNMINGDEKNSYECLIGPSTTTPTTTPTTTPTTTPTT----- 434
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                                                 536
                                                              142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 MHYYLNNGATRDKLVMGVPPYGRAWSIEDRSKVYLGDPAKGMSPPGFITGEEGYLSYIEL
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                                            GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cch 82.1%; Score 2475; DB 4; Length 509; al Similarity 82.5%; Pred. No. 1.3e-189; 443; Conservative 21; Mismatches 21; Indels 5
                                                                                                                                                    Sequence 38, Application US/09292225; Patent No. 6455686; GENERAL INFORMATION: APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Dermatophagoides farinae
US-09-292-225-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 443; Conserv
                                                                                                                       RESULT 6
US-09-292-225-38
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134 KKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQELRRAFIRVGKGWELTAAVPLANFR 193
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453 GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKANCIQE 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 QEYKFDGLDLDWEYPGSR-LGNPKIDKONYLALVRELKDAF--EPHGYLLTAAVSPGKDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
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                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kramer, Karl J.
APPLICANT: Muthukrishnan, Subbaratnam
APPLICANT: Choi, Hee Kyung
APPLICANT: Corpuz, Lolita
APPLICANT: Gopalakrishnan, Bhuvana
TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Length 583;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.0%; Score 812.5; DB 4; Best Local Similarity 35.6%; Pred. No. 1e-56; Matches 196; Conservative 86; Mismatches 197;
                                                                                                                     540
                                                                                              533
                                                                                                             VNGE--AMQFSCQHGTVFNVELNVC
                                                                                              509 VNGGWWVHIMPCPPGTIWCOEKLTC
                                                                                                                                                                    US-09-545-814-2
; Sequence 2, Application US/09545814
; Patent No. 6416977
                                                                     PKPEPQPEPEVEVP-PTENE---
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 583
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GAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------SYTVPPPHTENTTPTP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 IDRAYDIKELNKLFDWMNYMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 245
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                                                                                               -----TTPTTPS-----PTTPSPTTTPSPTTTPSPTTPSPTT------PT 450
                                                                                                                                              P-TTPTPAPTISTPSPTTTEHTSETPKYTTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEF 508
                                                GVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTFTTPT- 411
                                                                                                                       413 EWARPPSTPSDPSEGDPIPTTTAKPASTTKTTVKTTTTTTAKPPQSVIDEENDINVRPE 472
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                                                                                                                                                                                                                                                      RESULT 8
US-09-055-778-16
Sequence 16, Application US/09052778A
Sequence 16, Application US/09052778A
Sequence 16, Application US/09052778A
Settle No. 6060590
GENERAL INFORMATION:
APPLICANT: Bryant, Reter J.
APPLICANT: Kamamura, Kazuo
TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
TITLE OF INVENTION: OF USE
FILE REPREMENT OF USC
CURRENT APPLICATION NUMBER: US/09/052,778A
CURRENT APPLICATION NUMBER: US/09/052,778A
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 554
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                                                                                                                                                                                                                  VNGE--AMQFSCQHGTVFNVELNVC 540
                                                                                                                                                                                              VNGGWWVHIMPCPPGTIWCQEKLTC 533
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US-09-052-778-16
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                       450
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                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Becher, Anna M.
TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: PLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: O'SES THEREOF
FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: 0.000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PLING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSL
                                                                                     P-ITPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEF
                                                                                                                                  ------VDGSEI-CNSDQDYIPDKKHCDKYWRC--
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Sequence 14, Application US/09545814

Sequence 14, Application US/09545814

Patent No. 641697

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

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35.8%; Pred. No. 1.1e-56;
iive 86; Mismatches 193;
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; ORGANISM: Ctenocephalides felis
US-09-545-814-14
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Best Local Similarity
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   ---VHGEAV 525
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Becher, Anna M.

TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, FROTEINS AND TITLE OF INVENTION: USES THEREOF FILE SEPERANCE: FC-5-C1
CURRENT PRILIGATION NUMBER: US/09/545,814
CURRENT APPLICATION NUMBER: US/09/545,813
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 583
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478 HEEEKPSEQDNQVGSQDTTATD---VDCSQEDYLPH-EDCNKYYRC----
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; Pred. No. 1e-56;
86; Mismatches 197;
                                                                                                                                                                                                    RESULT 10
US-09-545-814-5
; Sequence 5, Application US/09545814
; Patent No. 6416977
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35.6%;
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Best Local Similarity 35.6
Matches 196; Conservative
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                                                                                                               526 LFTCREGTVY 535
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526 LFTCREGTVY 535
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APPLICANT: Becher,
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DGLDLDWEYPGSR-LGNPKIDKQNYLALVRELKDAFEPHG--YLLTAAVSPGKDKIDRAY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 KGHCG-PKNPLLNKVHNMINGDEKNSPECILGPSTTTPP--TTTPTTPTTTPTTPSPTT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTT-TPSPT-TPTTPSPTTTPSPTTPTPTTPAPTTSTPSPTTTB-----HTSET 474

    Sequence 32, Application US/09545814
    Patent No. 6416977
    GENERAL INFORMATION:

            APPLICANT: Becher, Anna M.
            TITLE OP INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-----KYTTYVDGHLIKCYKEGDI PHPINIHKYLVCEFVNGGWWVH----IMPCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 DIKELNKLFDWMNWMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDPSKGWTKKWDEHGKVPXAYKGNOWVGYEDPKSVALKMEFIKSKGYGGAMTWAIDMDDF
                                                                                                                     15 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                       74 EKRGYERFINILRLKNPELLTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKF
                                                                                                                                                                                                                                                                                                                                                                                             307 Q -- KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDF
                                                                                                                                                                           RIVCYPSNWAVYRPGIGRYGIEDIPVDLCTHIVYSFIGVDDKDWSVLVIDPELDIDDN--
                                                            Gaps
                                                            71;
Length 559;
                                                            Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 PSPTTPTTTPSPTTPTTPSPTTPT 450
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 PELEVP-KPGOPSEPEHGPSPGODT
                                                                                                                                                                                                               NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 34.2
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                                        amino acid
   New York
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: unk
                  COUNTRY: UN
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Sequence 4, Application US/08486839
Sequence 4, Application US/08486839
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                         129 QEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVRELKDAFEPHG--YLLTAAVSPGKDK 185
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                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                      Length 635;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                    26.9%; Score 809.5; DB 4;
35.6%; Pred. No. 2e-56;
tive 85; Mismatches 198;
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
FURBUT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 635
                                                                                                                                                                                  ) ORGANISM: Tagged Ctenocephalides felis US-09-545-814-32
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.6
Matches 196; Conservative
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US-08-486-839-4
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                                                                                                                                                                                                                                                                                         FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFFPHG-----YLLTAAVSPGKDK 185
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                                                                                                                                             71
                                                                                          15 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 73
                                                                                                                                                                                                                                                                                                                                                                                                                   310 KGATKORIQ-FKVPYIFRDNQWVGFDDVSFKTKVSYLKQKGLGGAMVWALDLDDPFA
                                                                                                                                                                                                                                                                                                                                                                                    186 IDRAYDIKELNKLFDWMVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHCGPKNPLLINKVHNMINGDEKNSFECILGPSTTTPTTTTTTTTPTTPSPTTPTTT
                                                                                                                       Length 466;
24.5%; Score 738; DB 2; Length 46
34.2%; Pred. No. 6.6e-51;
ive 85; Mismatches 150; Indels
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Patent No. 6057142
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A Human Chi
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US-09-039-198A-2
                    JS-09-039-198A-2
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TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases. UNMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 KGATKORIQ-DQ--KVPYIFRDNOWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAAVSPGKDK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------RYPLIQTLRQELSLPYLPSGN 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.5%; Score 738; DB 3; Length 466; 34.2%; Pred. No. 6.6e-51; Live 85; Mismatches 150; Indels
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                        NAME: Morriss, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
RELECOMMUNICATION INFORMATION:
TELLEPHONE: (516) 822-3550
TELLEFAX: (516) 822-3551
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELEVP-KPGOPSEPEHGPSPGODT 418
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                                                                                                                                                                                                                                                                SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                        New York
: United States of America
                                                                     ADDRESSEE: Hoffmann & Baron, LLP STREET: 6900 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.24
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3S: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                      ZIP: 11791
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 738; DB 3; Length 46; Pred. No. 6.6e-51; 85; Mismatches 150; Indels
Sequence 2, Application US/09039198A
Patent No. 6200351
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
TTTLE OF INTENTION: CHITINASE CHITIN-BINDING FRACMENTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,198A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Lauree, Li-Hsien
REGISTRATION NUMBER: 33,547
REPRENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%;
34.2%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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Search completed: March 22, 2004, 07:04:01 Job time : 44.2018 secs

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March 22, 2004, 06:42:54; Search time 44.7332 Seconds (without alignments) 640.518 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                         389414 seqs, 51625971 residues
                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      US-09-662-293-18
3107
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* 4.00

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		o ^A			SUMMARIES		
Result No.	Score	Query Match	Length	В	ΠD	Description	:
	3107	100.0	555	4	US-09-292-225-15	15,	Appl
N	3107	100.0	555	4	US-09-292-225-18	18,	Appl
m	3014	97.0	536	4	US-09-292-225-21	21,	Appl
4	2542	81.8	509	4	US-09-292-225-35	35,	Appl
Ŋ	2542	81.8	503	4	US-09-292-225-38	38,	Appl
w	2475	79.7	490	4	US-09-292-225-41	41	App1
7	838.5	27.0	554	~	US-08-524-051-2	'n	Appli
80	838.5	27.0	554	ო	US-09-052-778-16	9	App1
6	815.5	26.2	583	4	US-09-545-814-2	ď	ppli
10	815.5	26.2	583	4	US-09-545-814-5	ທ້	ppli
11	812.5	26.2	635	4	US-09-545-814-32	32	App1
12	811.5	26.1	559	4	US-09-545-814-14	14,	Appl
. 13	~	23.8	466	~	US-08-486-839-4	4, 4	ppli
14	738	23.8	466	m	US-09-151-011-4	4,	ppli
15	738	23:8	466	m	US-09-039-198A-2	'n	Appli
16	738	23.8	466	4	US-09-343-623-4	4,	ppli
17	738	23.8	466	4	US-08-877-599-2	'n	ppli
18	738	23.8	466	4	US-09-267-574-2	~	ppli
10	732.5	23.6	387	N	US-08-486-839-6	ý	ppli
20	732.5	23.6	387	ო	US-09-151-011-6	é,	Appli
21	732.5	23.6	387	4	US-09-343-623-6	ģ	ppli
22	732	23.6	466	ო	US-09-039-198A-4	4	Appli
23	732	23.6	466	4	US-08-877-599-4	4,	ppli
24	732	23.6	466	4	US-09-267-574-4	4	Appli
25	721.5	23.2	373	m	US-09-039-198A-14	14,	Appl
26	721.5	23.2	373	m	US-09-039-198A-15	12	Appl
27	721.5	23.2	373	4	US-08-877-599-14	Sequence 14, A	Appl

15, 15,	27.74	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13, Appl	Sequence 10, Appl Sequence 12, Appl Sequence 1, Appli Sequence 7, Appli	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
US-08-877-599-15 US-09-267-574-14 US-09-267-574-15	US-09-545-814-29 US-09-459-749D-17 US-08-694-915-2 US-08-694-915-4	US-08-850-348A-2 US-09-052-778-2 US-09-408-647A-2 US-09-052-778-13	US-07-939-501A-10 US-07-939-501A-12 US-07-939-501A-1 US-08-448-398-7	US-08-358-901-2 US-08-566-347-2 US-08-693-835-2
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ALIGNMENTS

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Sequence 15. Application US/0929225

| Sequence 15. Application US/0929225
| Sequence 15. Application US/0929225
| Patent NO. 6455666
| GENERAL INFORMATION:
| APPLICANT: McCall, Catherine A. APPLICANT: Weber, Eric R. TITLE OF INVENTION: NOVEL DERMATCHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF TITLE OF INVENTION: AND USES THEREOF TITLE OF INVENTION: AND USES THEREOF TITLE OF INVENTION: AND USES THEREOF TITLE OF INVENTION: NUMBER: US/09/292,225
| CURRENT APPLICATION NUMBER: 06/098,909 EARLIER APPLICATION NUMBER: 60/098,909 EARLIER FILING DATE: 1998-09-13
| EARLIER FILING DATE: 1998-09-13
| EARLIER FILING DATE: 1998-04-17
| RARLIER PILING DATE: 1998-04-17
| NUMBER OF SEQ ID NOS: 49
| SOFTWARE: PATENTING UNDER: 09/062,013
| EARLIER FILING DATE: 1998-04-17
| NUMBER OF SEQ ID NOS: 49
| SEQ ID NO 15
| LINGTH: 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTHLMYGRAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELFTMISLGGWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Dermatophagoides farinae US-09-292-225-15
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241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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                                                                                                                                                                            TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP
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                                                   241 PLYKRPDETDELHTYPNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA
                                                                                                                                   KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
                                                                                                                                                                                                                                                                      KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
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100.0%; Pred. No. 1.8e-233;
ive 0; Mismatches 0;
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Matches 536; Conservative
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US-09-292-225-21
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APPLICANT: MCCALINO:
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Wover DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REPREBENCE: AL-2-23
CURRENT APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER PILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,555
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION NUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
FARLIER FILING DATE: 1998-04-17
SOFTWARE: PALCATION VUMBER: 09/062,013
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   PLYKRPDETDELHTYFNVNYTWHYYLANGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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Best Local Similarity 100.0%; Score 3107; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.5e-241;
Matches 555; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09292225 Patent No. 6455686 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Dermatophagoides farinae
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Sequence 36, Application US/0929225

Patent No. 645566

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Mober, Eric R.
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: NOVER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER PILING DATE: 1998-06-13
EARLIER PILING DATE: 1998-06-13
EARLIER PILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/089,565
EARLIER APPLICATION NUMBER: 60/089,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
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EARLIER APPLICATION NUMBER: 00/082,013
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                                                       KCMSPPGFISGEEGVLSYIELCQLPQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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241 PLYKRPDETDELHTYFNVNYTMHYYLANGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300
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                                                                                      KGMSPPGFITGEEGVLSYIELCOLFOKEEWHIOYDEYYNAPYGYNDKIWVGYDDASISC
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                                                                                                                                                        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
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Best Local Similarity 81.7%; Pred. No. 1.1e-195;
Matches 456; Conservative 24; Mismatches 26;
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-38
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US-09-292-225-38
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Sequence 35, Application US/0929225

Patent No. 645566

GENERAL INPORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Meber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NUMBER: US/09/292, 225
CURRENT APPLICATION NUMBER: 60/098, 909
EARLIER APPLICATION NUMBER: 60/098, 909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-06-13
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49

SOFTWARE PATENTING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49

SOFTWARE PATENTING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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                                                                    241 YIWHYYLNNGATRDKLVWGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300
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                                  YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI
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81.7%; Pred. No. 1.1e-195;
ive 24; Mismatches 26;
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-35
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Best Local Similarity 81.7
Matches 456; Conservative
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243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKJKJQDPAKGMSPPGFITGEEGVLSYIEL 302
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          262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/524,051
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kramer, Karl J.
APPLICANT: Muthukrishnan, Subbaratnam
APPLICANT: Choi, Hee Kyung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-524-051-2
; Sequence 2, Application US/08524051
; Patent No. 586788
; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 2287
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEPHONE: (816)474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: [bic.]
TELEFAX: 101...
TELEFAX: 443-363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
""PE: amino acid
""PE: amino acid
""PE: amino acid
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Sequence 41, Application US/0929225

Patent No. 645566

GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES,

FILE REFERENCE: AL-2-C3

CURRENT APPLICATION NUMBER: US/09/292,225

CURRENT APPLICATION NUMBER: US/099,209

EARLIER APPLICATION NUMBER: 60/098,909

EARLIER FILING DATE: 1998-09-13

EARLIER FILING DATE: 1998-05-13

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-04-17

SEARLIER FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE PALENTIN Ver. 2.0
241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300
                                                                  KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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                                                                                                                                                                                                                                                                                                                                            435 ---PITIDSTSETPKYITYIDGHLIKCYKQGYLPHPIDVHKYLVCEYIATPNGGWWVHIM 491
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                                                                                                                                                                                361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP
                                                                                                                                                  KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
                                                                                                                                                                                                                                                                                                                    481 TPSPITTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF
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                                                                                                                                                                                                                                                                           421 TPTTPSTTSTTTPT-------
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Best Local Similarity 82.5%
Matches 443, Conservative
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US-09-292-225-41
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KDAF--BPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
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; ORGANISM: Ctenocephalides felis
US-09-545-814-2
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SOFTWARE: Patentin Ve
SEQ ID NO 2
LENGTH: 583
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MYGFAKI DEYKYTI QVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI SLGGWYEGSE
                                                                                                         184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP
                                                    KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL
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Patent No. 6060590

GENERAL INFORMATION:

APPLICANT: Bryant, Peter J.

APPLICANT: RAWAWHER, KARUNO

TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS

TITLE OF INVENTION: OF USE

FILE REFERENCE: 07306/15501

CURRENT APPLICATION NUMBER: US/09/052,778A

CURRENT FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 554
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US-09-052-778-16
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US-09-052-778-16
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291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCOLFOKEE--WHIOYDEYYNAPYGYNDKI 348
                                                                                                                                                                                                                                                                   290 NKEAGGGDPAPYTNATGF-----WAYYELCTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342
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TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND FILE REPERENCE: FC-5-C1
CURRENT PILLE REPERENCE: FC-5-C1
CURRENT PILLE DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
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RESULT 11
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                                                                                                              471
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                                            KEAGGGEPGPYTNATGFISYYEICLEVDDPSKGWTKKWDEHGKVPYAYKGNOWVGYEDPK 355
                                                                   SISCKLAFLKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGP 415
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                      PAKGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLA 356
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237 YRRPHD-QYAYEKLNVNDGLQLWVDMGCPANKLVVGVPFYGRSFTLSNSNKDYRLGTYIN 295
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Becher, Anna M.
TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
                                                                                                                              LLAVICAİAISSINTV----EASDQKARİVCYFSNWAVYRPGIGRYGIEDIPVDLCTHIV
                                                                                472 TPTPAPTTSTPSPTTTE-----HTSETP-----KYTTYVDGHLIKCYKEGDIPHPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 815.5; DB 4;
Pred. No. 3.6e-57;
                                                                                                                                                                                                          518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
                                                                                                                                                                                                                               ------VHGEAVLFTCREGTVY
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                , ORGANISM: Ctenocephalides felis
US-09-545-814-5
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Similarity 34.6%;
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SEQ ID NO 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 KEAGGGEPGPYINATGFISYYEICLEVDDFSKGWIKKWDEHGKVPYAYKGNQWVGYEDPK 356
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356 SVALKMEFIKSKGYGGAMTWAIDMDDFQGVCSDDKHTLAVIMHDYM----KNYIVPBFDS 411
                                                                                                                                                                       TPTPAPTTSTPSPTTTE----HTSETP-----KYTTYVDGHLIKCYKEGDIPHPT 517
                                                                                                                        SRITPRPEWAKPPSTPSQEP-DDTPYIPTHAPKPSRKPTRKPKPT--TTTVAATTPVAT 468
                                                                                                                                                                                                                    -------TriehhhhheekkeeQDNQVGSQDriato---VDCSQEDYLPH-E 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Becher, Anna M.

TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF FILE REPREBACE: PC-5-CURRENT PAPLICATION NUMBER: US/09/545,814

CURRENT APPLICATION NUMBER: 60/128,833

PRIOR APPLICATION NUMBER: 60/128,833

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEXRGYERFNNIRLKNPELTTMISLGGWYEGSEK
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 812.5; DB 4;
; Pred. No. 7e-57;
93; Mismatches 206;
                                                                                                                                                                                                                                                                                                        ::|| : | | : : | | 1:: : DCNKYYRC-----VHGEAVLFTCREGIVY 535
                                                                                                                                                                                                                                                                     518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-32
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09545814 Patent No. 6416977 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.69
Matches 198; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 32
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Mon

us-09-662-293-18.rai

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Sequence 14, Application US/09545814

Patent No. 6416977

GENERAL INFORMATION:
TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/09/545,814

CURRENT FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LENGTH: 559
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                   EKRGYERFINNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGLDLDWEYPGSR-LGNPKIDKQNYLALVRELKDAFEPHG--YLLTAAVSPGKDKIDRAY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 HVPELCELLDAIHVMSYDLRGNWAGFADTHSPLYRRPHD-CYAYEKLNVNDGLQLWVDMG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTT-TPSPT-TPTTTPSPTTTTTPSPTTPTTPTPTPAPTTSTPSPTTTE-----HTSET 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PITHAPKPSRKPTRKPKPI--TTTVAATIPVAI------TTTEHHHHHEEEK 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.1%; Score 811.5; DB 4; Length 559; Best Local Similarity 35.8%; Pred. No. 7.1e-57; Matches 195; Conservative 86; Mismatches 193; Indels 71
                                                            NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
                                                                                472 TPTPAPTTSTPSPTTTE----HTSETP
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Ctenocephalides felis
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US-09-545-814-14
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                                                                                 TITLE OF INVENTION: A human chitinabe, its recombinant III OF INVENTION: production, its use for decomposing chitin, its use IIILE OF INVENTION: in therapy or prophylaxis against infection diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFBPHG-----YLLTAAVSPGKDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.8%; Score 738; DB 2; Length 46
34.2%; Pred. No. 4.3e-51;
.ive 85; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE:
                                                                                                                                                                                                      CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Baron, Ronald J. REGISTRATION UNMERS: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
            Sequence 4, Application US/08486839
Patent No. 5928928
GENERAL INFORMATION:
                                                                                                                                                                        8: Hoffmann & Baron
350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (516) 822-3582 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 34.2 Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                      NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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TOPOLOGY: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                        ADDRESSEE:
STREET: 35
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US-08-486-839-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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----RYPLIQTLRQELSLPYLPSGT 394
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                                                                               310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDDFA
                                                           325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW
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Requence 2, Application US/09039198A

Replicant No. 6200951

APPLICANT: Gray, Patrick W.

APPLICANT: Tjocher, Larry W.

TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRACMENTS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower

CITY: Chicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/039,198A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.8%; Score 738; DB 3; 34.2%; Pred. No. 4.3e-51;
                                                                                                                                                                             --- FSCNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States of America
ZIP: 6006-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   PSPITTTTPSPITPTTTPSPITPT 469
                                                                                                                                                                                                                                                         PELEVP-KPGQPSEPEHGPSPGQDT
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ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
RECISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 2786(
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-630
TELEPHONE: (312) 474-6448
INFORMATION FOR SEQ ID NO: 2:
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amino acid
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US-09-039-198A-2
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                                     ---RYPLIQTLRQELSLPYLPSGT 394
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                                                                                                                                                                                                                                                                                         A Human Chitinase, Its Recombinant
Production, Its Use For Decomposing Chitin, Its Us
Therapy or Prophylaxis Against Infection Diseases.
 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTTPTTTPTTPTTPTTPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%; Score 738; DB 3; Length 466; 34.2%; Pred. No. 4.3e-51; Live 85; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                         ----FSCNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MOTTISS, ROBETT C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECOMMUNICATION INFORMATION:
                                                                             445 PSPTTPTTPSPTTPSPTTP 469
                                                                                                                 PELEVP-KPGQPSEPEHGPSPGQDT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Syosset
STATE: New York
COUNTXY: United States of America
ZIP: 11791
                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hoffmann & Baron, I
STREET: 6900 Jericho Turnpike
                                                                                                                                                                                                             Sequence 4, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 34.2*
Matches 152; Conservative
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TITLE OF INVENTION: A HUTITLE OF INVENTION: Prodring of INVENTION: The NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3S: unknown
unknown
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                                   367 G----
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                                                                                                                   395
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Db 191 UDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324

Db 250 WLQXGTPASKLILGMFTYGRSFTLASSSDTRVGAPPGFISGEEGVLSYYEVCSW 309

Cy 325 FQKEEWHIQYDEYTNAPYGYNDKIWYGYDDLASISCKLAFLKELGVSGWYWSLENDDFK 384

Db 310 KGATKQRIQ-DQ--KVPYIFRDNQWYGFDDVESFKTKVSKGLGGAMVWALDLDDFR 366

Cy 385 GHCGPKNPLINKVHNMINGDEKNSFECILGPSTTTPTTTTPTTTPTTTPTTTPTTTT 444

Db 367 G--------FSCNQG-------RYPLIGTLRQELSLPYLPSGT 394

CY 445 PSPTTPTTTPSPTTPT 469

DD 395 PELEVP-KPQQPSEPEHGPSPGQDT 418

Search completed: March 22, 2004, 07:04:00

JOD time: 46.7332 secs
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